

Result No.	Score	Query Match	Length	DB	ID	Description	
1	3026	100.0	560	2	AAW35382	Murine me	
2	3026	100.0	560	3	AAB11329	Human lun	
3	3026	100.0	560	5	ABb78200	Amino aci	
4	3026	100.0	560	5	ABb74961	Human lun	
5	3026	100.0	560	5	ABPe1881	Human lun	
6	3026	100.0	560	6	ABU56592	Lung canc	
7	3026	100.0	560	6	ABg72962	Human ost	
8	3026	100.0	560	6	ABU70852	Human adi	
9	3026	100.0	560	7	ADA28315	Human lun	
10	3026	100.0	560	7	ADe95620	Human NOV	
11	3026	100.0	560	7	ADH36879	Human lun	
12	3026	100.0	560	7	ADJ68660	Human hea	
13	3026	100.0	560	7	ADL14995	Human NMB	
14	3026	100.0	560	7	ADN39940	Cancer/an	
15	3026	100.0	560	8	ADH56342	Human nmb	
16	3026	100.0	560	8	ADJ75569	Marker ge	
17	3026	100.0	560	8	ADG56682	Human lun	
18	3026	100.0	560	8	ADQ18310	Human sof	
19	3007	99.4	572	7	ADD78235	Human CGD	
20	3006	99.3	572	5	AuA83612	Human PRO	
21	3006	99.3	572	6	ABU80759	Human PRO	
22	3006	99.3	572	6	ABO33725	Novel hum	
23	3006	99.3	572	6	ABU82068	Novel hum	
24	3006	99.3	572	6	ABJ72248	Human PRO	
25	3006	99.3	572	6	ABJ72376	Human PRO	

CC expression product may also be used to treat a metastatic disorder

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.7e-262;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFGLGFLAARLPDAAKRFHDLGNRPSAYMRHNLQNGSSDENDWNEKLYP 60  
Db 1 MECLYFGLGFLAARLPDAAKRFHDLGNRPSAYMRHNLQNGSSDENDWNEKLYP 60  
QY 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVVEKNC 120  
Db 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVVEKNC 120  
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDDGKPPPHHGWRRWNPYYVFTL 180  
Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDDGKPPPHHGWRRWNPYYVFTL 180  
QY 181 GQYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVTV 240  
Db 181 GQYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVTV 240  
QY 241 TWFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
Db 241 TWFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360  
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360  
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVCTIISDPT 420  
Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVCTIISDPT 420  
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
QY 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLKNQEFKGV 560  
Db 541 FPGNQEKDPLLKNQEFKGV 560

## RESULT 2

AAB11329  
ID AAB11329 standard; protein; 560 AA.

XX AC AAB11329;

XX DT 21-FEB-2001 (first entry)

XX DE Human lung cancer-associated protein L528S.

XX KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
XX KW vaccine; detection.

XX OS Homo sapiens.

XX FN WO2000061612-A2.

XX PD 19-OCT-2000.

XX PF 03-APR-2000; 2000WO-US008896.

XX PR 02-APR-1999; 99US-00285479.

XX PR 17-DEC-1999; 99US-00466396.

XX PR 30-DEC-1999; 99US-00476496.

PR 10-JAN-2000; 2000US-00480884.  
PR 22-FEB-2000; 2000US-00510376.

PA (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor  
PT protein is used for detecting and monitoring progression of lung cancer  
PT in a patient.

PS Claim 3; Page 203-204; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which  
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)  
CC which have cytostatic activity. The polypeptides and polynucleotides are  
CC used in compositions and vaccines to inhibit the development of cancer,  
CC especially lung cancer, in a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 3; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYFGLGFLAARLPDAAKRFHDLGNRPSAYMRHNLQNGSSDENDWNEKLYP 60  
Db 1 MECLYFGLGFLAARLPDAAKRFHDLGNRPSAYMRHNLQNGSSDENDWNEKLYP 60  
QY 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVVEKNC 120  
Db 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCQKEDANGNIVVEKNC 120  
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDDGKPPPHHGWRRWNPYYVFTL 180  
Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFDDGKPPPHHGWRRWNPYYVFTL 180  
QY 181 GQYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVTV 240  
Db 181 GQYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVVVTDOIPVTV 240  
QY 241 TWFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
Db 241 TWFQKNDNRNSDETFLKDLPIFMDVLIHDPHSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360  
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLESRIIPDENCQIN 360  
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVCTIISDPT 420  
Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVCTIISDPT 420  
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
QY 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PLRMANSALISVGCIAIFVTVISLLVYKHKKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLKNQEFKGV 560  
Db 541 FPGNQEKDPLLKNQEFKGV 560

	Query Match	100.0%	Score 3026;	DB 5;	Length 560;
	Best Local Similarity	100.0%;	Pred. No. 4.7e-262;		
	Matches 560;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MECLYYELGFLLLAARLPDAAKEFHVDLGNRPSAYMREHNQNGSSDENDWNEKLYP	60		
Db	1	MECLYYELGFLLLAARLPDAAKEFHVDLGNRPSAYMREHNQNGSSDENDWNEKLYP	60		
Qy	61	VWKEGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC	120		
Db	61	VWKEGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC	120		

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PS Disclosure; Page 281-283; 374pp; English.
XX
CC The present invention describes human lung tumour proteins. Human lung
CC tumour proteins and polynucleotides have cytostatic and immunostimulant
CC activities, and can be used in vaccine production. Compositions
CC comprising the lung tumour proteins, polynucleotides, antibodies, fusion
CC proteins, T cell populations, or antigen presenting cells that express
CC the lung tumour proteins are useful for treating lung cancer or
CC stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to
CC ABB75070 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 560 AA;
Query Match 100.0%; Score 3026; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDGPFPHPGWRWNFIYVFTL 180
Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDGPFPHPGWRWNFIYVFTL 180
QY 181 GOYFQKLGRCVRSVSVNTANVTLPQMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPVFV 240
Db 181 GOYFQKLGRCVRSVSVNTANVTLPQMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPVFV 240
QY 241 TMFQKNDNRSSDTEFLKDLPIFMDVLIHDPSEFLNVTINYNKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDTEFLKDLPIFMDVLIHDPSEFLNVTINYNKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLNLTAKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360
Db 301 HTYVLNGTFSNLNLTAKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420
Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDENCLLTVRTFNGSGTYCVNLTLGDDTSLALTSTLISVPDRDPAS 480
Db 421 CEITQNTVCSVDVDENCLLTVRTFNGSGTYCVNLTLGDDTSLALTSTLISVPDRDPAS 480
QY 481 PLRMANSALISVGLAIFVTVISLLYKKGKEYNPINSPGNVVRSGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGLAIFVTVISLLYKKGKEYNPINSPGNVVRSGLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLNKQEFKGV 560
Db 541 FPGNQEKDPLLNKQEFKGV 560
RESULT 5
ABP61881
ID ABP61881 standard; protein; 560 AA.
XX
AC ABP61881;
XX
XX 07-OCT-2002 (first entry)
XX
DE Human lung cancer associated protein sequence SEQ ID NO:225.
XX
XX Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
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PN WO200247534-A2.
XX
XX 20-JUN-2002.
XX
XX 30-NOV-2001; 2001WO-US047576.
XX
XX 12-DEC-2000; 2000US-00735705.
XX
XX 07-MAY-2001; 2001US-00850716.
XX
XX 28-JUN-2001; 2001US-00897778.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;
XX McNeill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;
XX Carter D, Watanabe Y, Peckham DW, Cai F, Foy TM;
XX WPI; 2002-583465/62.
XX
XX Novel lung carcinoma polynucleotide sequences and polypeptides encoded by
XX the polynucleotides, useful in pharmaceutical compositions such as
XX vaccines and as markers to indicate the presence of lung cancer.
XX
XX Example 1; Page 289-290; 381pp; English.
XX
XX The present invention describes isolated human lung carcinoma
XX polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic
XX activity, and can be used in gene therapy and in vaccines. Compositions
XX comprising (I) or (II) can be used for stimulating an immune response in
XX a patient and for treating lung cancer in a patient. Oligonucleotides of
XX (I) can be used for detecting the presence of a cancer in a patient, by
XX obtaining a biological sample from the patient, contacting the biological
XX sample with the oligonucleotide, detecting in the sample, an amount of
XX polynucleotide that hybridises to the oligonucleotide and comparing the
XX amount of polynucleotide that hybridises to the oligonucleotide to a
XX predetermined cut-off value, and determining the presence of a cancer in
XX the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.
XX vaccines. (I) is useful as a marker to indicate the presence or absence
XX of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to
XX ABP61992 represent sequences used in the exemplification of the present
XX invention
XX
XX Sequence 560 AA;
Query Match 100.0%; Score 3026; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDLGNRPSAYMRHNLNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFPRCKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDGPFPHPGWRWNFIYVFTL 180
Db 121 RNEAGLSADPYVYNWTAWSEDSGNGTQSHHNVFPDGPFPHPGWRWNFIYVFTL 180
QY 181 GOYFQKLGRCVRSVSVNTANVTLPQMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPVFV 240
Db 181 GOYFQKLGRCVRSVSVNTANVTLPQMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPVFV 240
QY 241 TMFQKNDNRSSDTEFLKDLPIFMDVLIHDPSEFLNVTINYNKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDTEFLKDLPIFMDVLIHDPSEFLNVTINYNKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLNLTAKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360
Db 301 HTYVLNGTFSNLNLTAKAAPGCPPPPPTSPKPTPSLGPAGDNPLELSRIEDNCQIN 360
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420
Db 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCQSIPTEVCTIISDPT 420
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Db 361 RYGHFOATITIVGILEVNI IQMTDVLMPVPPESSLDIFVTCQGSIPTEVCTIISDPT 420  
Qy 421 CEITQNTVCS PVDVDEMCLLIVRTFNGSGTYCVNLTLGGDTSLALTSTLISVPRDRPAS 480  
Db 421 CEITQNTVCS PVDVDEMCLLIVRTFNGSGTYCVNLTLGGDTSLALTSTLISVPRDRPAS 480  
Qy 481 PLRMANSALISVGCLAI FVTVISLVYKKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PLRMANSALISVGCLAI FVTVISLVYKKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540  
Qy 541 FPGNQEKDPLLNQEFKGV 560  
Db 541 FPGNQEKDPLLNQEFKGV 560

## RESULT 6

ID ABUS6592 standard; protein; 560 AA.  
XX

AC ABUS6592;  
XX

DT 02-APR-2003 (first entry)  
XX

XX Lung cancer-associated polypeptide #185.  
XX

KW Lung cancer-associated polypeptide; cytostatic; emphysema;  
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
XX

OS Unidentified.  
XX

XX WO200286443-A2.  
XX

XX 31-OCT-2002.  
XX

XX 18-APR-2002; 2002WO-US012476.  
XX

XX 18-APR-2001; 2001US-0284770P.  
XX

XX 10-MAY-2001; 2001US-0290492P.  
XX

XX 09-NOV-2001; 2001US-0339245P.  
XX

XX 13-NOV-2001; 2001US-0350666P.  
XX

XX 29-NOV-2001; 2001US-0334370P.  
XX

XX 12-APR-2002; 2002US-0372246P.  
XX

XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX

XX Aziz N, Murray R;  
XX

XX WPI; 2003-093161/08.  
XX

XX N-PSDB; ABX76321.  
XX

XX Detecting a lung cancer-associated transcript in a cell from a patient  
XX for treating lung cancer, by contacting a biological sample from the  
XX patient with a polynucleotide that exhibits increased or decreased  
XX expression in lung cancer.  
XX

XX Claim 27; Page 328; 453pp; English.  
XX

XX The invention relates to a method for detecting a lung cancer-associated  
XX transcript in a cell from a patient, comprising contacting a biological  
XX sample from the patient with a polynucleotide that selectively hybridises  
XX to a sequence that is at least 80 % identical to a gene that exhibits  
XX increased or decreased expression in lung cancer samples. Lung cancer-  
XX associated polynucleotides and polypeptides are used for identifying a  
XX compound that modulates a lung cancer-associated polypeptide, for  
XX inhibiting proliferation of a lung cancer-associated cell to treat lung  
XX cancer in a patient and for treating a mammal having lung cancer by  
XX administering a modulatory compound identified. The methods are useful  
XX for treating lung cancer, such as small cell lung cancer, non-small cell  
XX lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
XX emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the  
CC invention  
XX

SQ Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 6; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECLYFFLGFLLLAARLPDAAKRFHDLGNERPSAYMRHNQLNGWSSDENDWNEKLYP 60

Db 1 MECLYFFLGFLLLAARLPDAAKRFHDLGNERPSAYMRHNQLNGWSSDENDWNEKLYP 60

Qy 61 VKRGDMWKNSWKGGRVQAVLTSDSPALVGSNTTFAVNLIFPRCKEDANGNIYKNC 120

Db 61 VKRGDMWKNSWKGGRVQAVLTSDSPALVGSNTTFAVNLIFPRCKEDANGNIYKNC 120

Qy 121 RNEAGLSADPYVYNWTAMSEDSGNGTGQSHHNVFPDGKPPHPHGRWRNFIYVHTL 180

Db 121 RNEAGLSADPYVYNWTAMSEDSGNGTGQSHHNVFPDGKPPHPHGRWRNFIYVHTL 180

Qy 181 GQYFQKLGRCVRSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTQDQIPVFV 240

Db 181 GQYFQKLGRCVRSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTQDQIPVFV 240

Qy 241 TMFQKNDKNSDDETFKDLPTIMEDVLIHDPSEFLNYSTINYNKWSFGDNTGLFVSTNHTVN 300

Db 241 TMFQKNDKNSDDETFKDLPTIMEDVLIHDPSEFLNYSTINYNKWSFGDNTGLFVSTNHTVN 300

Qy 301 HTYVLNGTFSNLNLTAKAAAGCPPPPPPPPSKPTPSLGPAGDNPLESLRIPDENCIN 360

Db 301 HTYVLNGTFSNLNLTAKAAAGCPPPPPPPPSKPTPSLGPAGDNPLESLRIPDENCIN 360

Qy 361 RYGHFOATITIVGILEVNI IQMTDVLMPVPPESSLDIFVTCQGSIPTEVCTIISDPT 420

Db 361 RYGHFOATITIVGILEVNI IQMTDVLMPVPPESSLDIFVTCQGSIPTEVCTIISDPT 420

Qy 421 CEITQNTVCS PVDVDEMCLLIVRTFNGSGTYCVNLTLGGDTSLALTSTLISVPRDRPAS 480

Db 421 CEITQNTVCS PVDVDEMCLLIVRTFNGSGTYCVNLTLGGDTSLALTSTLISVPRDRPAS 480

Qy 481 PLRMANSALISVGCLAI FVTVISLVYKKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540

Db 481 PLRMANSALISVGCLAI FVTVISLVYKKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540

Qy 541 FPGNQEKDPLLNQEFKGV 560

Db 541 FPGNQEKDPLLNQEFKGV 560

## RESULT 7

ABG72962

ID ABG72962 standard; protein; 560 AA.

XX AC ABG72962;

XX AC ABG72962;

XX DT 08-APR-2003 (first entry)

XX Human osteoactivin homologue, nmb.

XX Human; osteoactivin; osteopathic; antiinflammatory; vaccine;

XX bone cell differentiation stimulator; gene therapy; bone formation;

XX osteoporosis; periodontal disease; ectopic bone formation; osteopetrosis;

XX bone disorder; osteogenesis; enzyme.

XX Homo sapiens.

XX OS

XX US2002151486-A1.

XX PN

XX XX

PD 17-OCT-2002.  
XX  
XX 30-AUG-2001; 2001US-00943075.  
XX  
XX 30-AUG-2000; 2000US-0229006P.  
PR  
XX (POPO/) POPOFF S N.  
PA (SAFA/) SAFADI F F.  
PA (OWEN/) OWEN T A.  
PA (SMOC/) SMOCK S L.  
XX  
PI Popoff SN, Safadi FF, Owen TA, Smock SL;  
XX WPI; 2003-182528/18.  
DR  
XX  
XX Novel isolated osteoactivin protein and gene encoding the protein, useful  
PT for stimulating bone differentiation and for treating bone disorders  
PT including osteoporosis and periodontal disease.  
PT  
XX  
XX Claim 24; Fig 2B; 38pp; English.  
PS  
XX The invention describes an isolated and substantially pure osteoactivin  
CC protein (I) that stimulates bone cell differentiation. A therapeutic  
CC composition comprising (I), the polynucleotide (I) encoding (I) or a  
CC biologically active fragment of (I) is useful for stimulating bone  
CC formation in a mammal. The composition is also useful for treating a bone  
CC disorder including osteoporosis and periodontal disease. A second  
CC therapeutic composition comprising an anti-(I)-antibody or an agent that  
CC inhibits osteoactivin-mediated bone formation is also useful for inhibiting  
CC formation in a mammal. The second composition is also useful for treating  
CC ectopic bone formation and osteopetrosis. (I) and (II) are also useful  
CC for developing novel therapeutic compositions for bone disorders, and for  
CC stimulating osteogenesis. The polynucleotide is also useful in gene  
CC therapy. This is the amino acid sequence of human mmb, a homologue of the  
CC rat osteoactivin of the invention used in the creation of antibodies for  
CC detection of mmb and osteoactivin  
XX  
XX Sequence 560 AA;  
SQ  
Query Match 100.0%; Score 3026; DB 6; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.7e-262;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYYFLGFLLLAARLPDAAKRFHVDVIGNERPSPAYMRHNLGWSDDNDWNEKLYP 60  
DB 1 MECLYYFLGFLLLAARLPDAAKRFHVDVIGNERPSPAYMRHNLGWSDDNDWNEKLYP 60  
QY 61 VKRGRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120  
DB 61 VKRGRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC 120  
QY 121 RNEAGLSADPYVYNWTAWSEDSGNGTGSHHNVFDPGKPPHHPGWRWNPIYVPHTL 180  
DB 121 RNEAGLSADPYVYNWTAWSEDSGNGTGSHHNVFDPGKPPHHPGWRWNPIYVPHTL 180  
QY 181 GQYFQKLGRCSVRVSVNTAVNTLGPOLMEVTVYRRGAVPTAOKVDVYVTDQIPVFV 240  
DB 181 GQYFQKLGRCSVRVSVNTAVNTLGPOLMEVTVYRRGAVPTAOKVDVYVTDQIPVFV 240  
QY 241 TMFQKNDRNSDRTFLKDLPIFMDVLIHDPSPFLNTSTINYKWSFGDNTGLFVSTNHTVN 300  
DB 241 TMFQKNDRNSDRTFLKDLPIFMDVLIHDPSPFLNTSTINYKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTYVLNGTSLNLTVAAGAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIDENCQIN 360  
DB 301 HTYVLNGTSLNLTVAAGAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIDENCQIN 360  
QY 361 RYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIVVTCQGISIPEVCTIISDPT 420  
DB 361 RYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIVVTCQGISIPEVCTIISDPT 420  
QY 421 CEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLISVPRDRPAS 480  
DB 421 CEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLISVPRDRPAS 480  
QY 481 PLRMANSALISVGCCLAIFVTVISLVYKKGKYNPIENSPGNVRSKGLSVFLNRAKAYF 540  
DB 481 PLRMANSALISVGCCLAIFVTVISLVYKKGKYNPIENSPGNVRSKGLSVFLNRAKAYF 540  
QY 541 PFGNQEKOPLLKNQEFKGSV 560  
DB 541 PFGNQEKOPLLKNQEFKGSV 560  
RESULT 8  
ABU70852  
ID ABU70852 standard; protein; 560 AA.  
XX  
XX AC ABU70852;  
XX  
XX DT 10-JUN-2003 (first entry)  
XX  
XX DE Human adipocyte Selected Interacting domain, SID, #483.  
XX  
XX Human; prey; adipocyte; SID; selected interacting domain; anorectic;  
KW antidiabetic; protein-protein interaction; diabetes;  
KW yeast 2-hybrid assay; metabolic disorder; obesity.  
XX  
XX OS Homo sapiens.  
XX  
XX WO200286122-A2.  
XX  
XX PD 31-OCT-2002.  
XX  
XX PF 14-MAR-2002; 2002WO-EP003768.  
XX  
XX PR 14-MAR-2001; 2001US-0275734P.  
XX  
XX PA (HYBR-) HYBRIGENICS.  
XX  
XX PI Legrain P, Daviet L;  
XX  
XX WPI; 2003-103412/09.  
DR N-PSDB; ACA57396.  
XX  
XX New complex between two interacting proteins in adipocyte cells, useful  
PT for identifying selected interacting domains that modulate protein  
PT interactions, or for preventing or treating metabolic disorders such as  
PT obesity or diabetes.  
XX  
XX Claim 6; Page 269-270; 382pp; English.  
XX  
XX The invention relates to a complex between two interacting proteins in  
CC adipocyte cells, given in the specification. The proteins are identified  
CC by selecting a bait protein from a known adipocyte marker and then  
CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by  
CC members of an adipocyte cDNA library. The proteins are designated SID  
CC (RTM) (selected interacting domains) proteins. Also included are a  
CC polynucleotide encoding a polypeptide in the adipocyte cells, a  
CC recombinant host cell expressing at least one of the interacting  
CC polypeptides of the complex, selecting a modulating compound in adipocyte  
CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid  
CC sequences given in the specification (including its fragment or variant),  
CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences  
CC given in the specification (including its fragment or variant), a vector  
CC comprising the SID (RTM) polynucleotide, a recombinant host cell  
CC comprising the vector, a protein chip comprising the polypeptides and a  
CC record comprising all or part of the data, listed in the specification.  
CC The complex, polypeptides, polynucleotides and compounds are useful for  
CC preventing or treating metabolic disorders such as obesity or diabetes.  
CC The polynucleotides are useful as probes or primers. The complex is  
CC particularly useful for identifying selected interacting domains (SID  
CC (RTM)) for screening drugs that modulate the protein interaction, thus  
CC exhibiting the therapeutic effect. The present sequence represents a SID  
XX (prey) protein of the invention

```

SQ Sequence 560 AA;
Query Match 100.0%; Score 3026; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.7e-262;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMREHNLQNGWSSDENDWNEKLYP 60
DB 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMREHNLQNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120
DB 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDGNGTQSHNVFPDGKPFPHPGWRWNFIYVPHTL 180
DB 121 RNEAGLSADPYVYNWTAWSESDGNGTQSHNVFPDGKPFPHPGWRWNFIYVPHTL 180
QY 181 GOYFQKLGRCSVRSVNTANVTLGQPMEDVLIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 240
DB 181 GOYFQKLGRCSVRSVNTANVTLGQPMEDVLIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 240
QY 241 TMFQKNDNRNSDTEFLKDLPIKMPDVLIIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRNSDTEFLKDLPIKMPDVLIIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFTSLNLTVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCOIN 360
DB 301 HTYVLNGTFTSLNLTVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCOIN 360
QY 361 RYGHFOATTITVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVECTIISDPT 420
DB 361 RYGHFOATTITVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVECTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLIVRTFTNGSGTYCVNLTGLDDTSLALTSLISVPRDRPAS 480
DB 421 CEITQNTVCSVDVDEMCLLIVRTFTNGSGTYCVNLTGLDDTSLALTSLISVPRDRPAS 480
QY 481 PLRMANSALISVGLAIKFTVTISLLVKKHKEYNPIENSPGNVRSKLSVFLNRAKAVF 540
DB 481 PLRMANSALISVGLAIKFTVTISLLVKKHKEYNPIENSPGNVRSKLSVFLNRAKAVF 540
QY 541 FPGNQEKDPLLNQEFKGV 560
DB 541 FPGNQEKDPLLNQEFKGV 560

RESULT 9
ADA28315
ID ADA28315 standard; protein; 560 AA.
XX
AC ADA28315;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human lung tumour I528S protein.
XX
KW cancer; lung cancer; gene therapy; vaccine; human;
KW lung squamous cell carcinoma.
XX
OS Homo sapiens.
XX
FN US2003064947-A1.
XX
PD 03-APR-2003.
XX
FF 30-NOV-2001; 2001US-00007700.
XX
PR 18-MAR-1998; 98US-00040802.
PR 27-JUL-1998; 98US-0012312.
PR 22-DEC-1998; 98US-00221107.
PR 02-APR-1999; 99US-00285479.
PR 17-DEC-1999; 99US-00466396.

```

30-DEC-1999; 99US-00476496.  
10-JAN-2000; 2000US-00480884.  
22-FEB-2000; 2000US-00510376.  
04-APR-2000; 2000US-00542615.  
28-JUN-2000; 2000US-00606421.  
02-AUG-2000; 2000US-00630940.  
21-AUG-2000; 2000US-00643597.  
15-SEP-2000; 2000US-00662786.  
09-OCT-2000; 2000US-00685696.  
12-DEC-2000; 2000US-00735705.  
07-MAY-2001; 2001US-00850716.  
28-JUN-2001; 2001US-00897778.  
(CORI-) CORIXA CORP.  
Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderson RA;  
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR, Vedvick TS;  
Carter D, Watanabe Y, Peckham DW, Cal F, Foy TW;  
WPI; 2003-540798/51.  
New isolated polynucleotides and polypeptides useful for diagnosing,  
preventing and/or treating cancer, particularly lung cancer.  
Example 7; Page 194-195; 296pp; English.  
The invention describes isolated polynucleotides and polypeptides useful  
for diagnosing, preventing and/or treating cancer, particularly lung  
cancer. A new isolated polynucleotide comprises: any of the 22 fully  
defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the  
specification; complements of the nucleotide sequences cited above; at  
least 10 contiguous residues of the nucleotide sequences cited above; a  
sequence that hybridise to any of the nucleotide sequences under highly  
stringent conditions; a sequence that is at least 75 or 90% identical to  
the above nucleotide sequences; or degenerate variants of the above  
nucleotide sequences. The composition and methods are useful in  
diagnosing, preventing and/or treating cancer, particularly lung cancer,  
in gene therapy and in vaccines. This is the amino acid sequence encoded  
by a human lung tumour cDNA isolated from a lung squamous cell carcinoma  
that may be useful in the diagnosis and treatment of lung cancer and  
other disorders.  
Sequence 560 AA;  
Query Match 100.0%; Score 3026; DB 7; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.7e-262;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMREHNLQNGWSSDENDWNEKLYP 60  
DB 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNERPSAYMREHNLQNGWSSDENDWNEKLYP 60  
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
DB 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
QY 121 RNEAGLSADPYVYNWTAWSESDGNGTQSHNVFPDGKPFPHPGWRWNFIYVPHTL 180  
DB 121 RNEAGLSADPYVYNWTAWSESDGNGTQSHNVFPDGKPFPHPGWRWNFIYVPHTL 180  
QY 181 GOYFQKLGRCSVRSVNTANVTLGQPMEDVLIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 240  
DB 181 GOYFQKLGRCSVRSVNTANVTLGQPMEDVLIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 240  
QY 241 TMFQKNDNRNSDTEFLKDLPIKMPDVLIIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300  
DB 241 TMFQKNDNRNSDTEFLKDLPIKMPDVLIIHDPHSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTYVLNGTFTSLNLTVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCOIN 360  
DB 301 HTYVLNGTFTSLNLTVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCOIN 360  
QY 361 RYGHFOATTITVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVECTIISDPT 420  
DB 361 RYGHFOATTITVEGILEVNIQMTDVLMPVPWPESSLDIFVVTCCGSIPTVECTIISDPT 420  
QY 421 CEITQNTVCSVDVDEMCLLIVRTFTNGSGTYCVNLTGLDDTSLALTSLISVPRDRPAS 480  
DB 421 CEITQNTVCSVDVDEMCLLIVRTFTNGSGTYCVNLTGLDDTSLALTSLISVPRDRPAS 480  
QY 481 PLRMANSALISVGLAIKFTVTISLLVKKHKEYNPIENSPGNVRSKLSVFLNRAKAVF 540  
DB 481 PLRMANSALISVGLAIKFTVTISLLVKKHKEYNPIENSPGNVRSKLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLNQEFKGV 560  
DB 541 FPGNQEKDPLLNQEFKGV 560

Db 361 RYGHFQATITVEGLEVINIQTMDVLPVMPPESSLIIDFVVTCQSGIPTVECTIISDPT 420  
Qy 421 CEITQNTVCSPVDVDEMCLLTVRRFTFNGSGTYCVNLTGLGDDTSLATSTLISVPRDRPAS 480  
Db 421 CEITQNTVCSPVDVDEMCLLTVRRFTFNGSGTYCVNLTGLGDDTSLATSTLISVPRDRPAS 480  
Qy 481 PLRMANSLISVGLCLAFVTIVSLVYKHKKEYNPIENSGNVVRSGKLSVFLNRAKAVF 540  
Db 481 PLRMANSLISVGLCLAFVTIVSLVYKHKKEYNPIENSGNVVRSGKLSVFLNRAKAVF 540  
Qy 541 PFGNQEKDPLLNQEFKGV 560  
Db 541 PFGNQEKDPLLNQEFKGV 560  
RESULT 10  
ADE95620  
ID ADE95620 standard; protein; 560 AA.  
AC ADE95620;  
DT 12-FEB-2004 (first entry)  
XX Human NOVX28c protein.  
XX NOVX protein; biochemical stimulation; physiological stimulation;  
KW cardiant; antiatherosclerotic; hypotensive; cytostatic; anorectic;  
KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;  
KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;  
KW nootropic; antipsoriatic; antiparkinsonian; antiashtmatic; neuroleptic;  
KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;  
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;  
KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;  
KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;  
KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;  
KW depression; allergy; fertility disorder; NOVX28c.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 47  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Arg as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 57  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Glu as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 111  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Asp as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 130  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Pro as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 154  
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FT /note= "OTHER= May be substituted by Ser as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 162  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Leu as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 294  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Phe as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 324  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Leu as a result of a  
FT single nucleotide polymorphism"

FT Misc-difference 460  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Asp as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 487  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Ser as a result of a  
FT single nucleotide polymorphism"  
FT Misc-difference 526  
FT /label= OTHER  
FT /note= "OTHER= May be substituted by Arg as a result of a  
FT single nucleotide polymorphism"  
WO2003050245-A2.  
19-JUN-2003.  
03-DEC-2002; 2002WO-US038594.  
05-DEC-2001; 2001US-0336600P.  
07-DEC-2001; 2001US-0338285P.  
12-DEC-2001; 2001US-0341346P.  
17-DEC-2001; 2001US-0341477P.  
17-DEC-2001; 2001US-0341540P.  
20-DEC-2001; 2001US-0342592P.  
27-DEC-2001; 2001US-0344297P.  
31-DEC-2001; 2001US-0344903P.  
17-APR-2002; 2002US-0373286P.  
15-MAY-2002; 2002US-0380981P.  
17-MAY-2002; 2002US-0381495P.  
28-MAY-2002; 2002US-0383534P.  
28-MAY-2002; 2002US-0383744P.  
29-MAY-2002; 2002US-0383829P.  
29-MAY-2002; 2002US-0384024P.  
07-AUG-2002; 2002US-0401788P.  
26-OCT-2002; 2002US-0406353P.  
31-OCT-2002; 2002US-00401788.  
02-DEC-2002; 2002US-00406353.  
(CURA-) CURAGEN CORP.  
Xx  
Xx Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;  
Xx Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;  
Xx Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphey R;  
Xx Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenoy SG;  
Xx Smithson G, Stirling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;  
Xx WPI; 2003-513974/48.  
Xx N-PSDB; ADE95619.  
Xx New NOVX polypeptides and nucleic acids, useful for preventing or  
Xx treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
Xx atherosclerosis or diabetes, and in chromosome mapping, tissue typing or  
Xx pharmacogenomics.  
Xx Claim 2; SEQ ID NO 152; 211pp; English.  
Xx This invention relates to novel NOVX proteins, and the DNA sequence which  
Xx encode them, having properties related to stimulation of biochemical or  
Xx physiological responses in a cell, a tissue, an organ or an organism.  
Xx Compounds which modulate the proteins of the invention may have cardiant,  
Xx antiatherosclerotic, hypotensive, cytostatic, anorectic, antirheumatic,  
Xx antiarthritic, antidiabetic, nephrotropic, dermatological,  
Xx immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,  
Xx nootropic, antipsoriatic, antiparkinsonian, antiashtmatic, neuroleptic,  
Xx antidepressant, antiallergic or gynaecological activities. The DNA  
Xx sequences of the invention may be useful for gene therapy whilst the  
Xx protein sequences may allow the development of a vaccine. The protein is  
Xx useful in the manufacture of a medicament for treating a syndrome  
Xx associated with a human disease. The invention may be useful in  
Xx diagnosing, treating or preventing NOVX-associated disorders, for example  
Xx cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,  
Xx rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin



CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,  
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or  
 CC fertility disorders. The nucleic acids may further be used as  
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
 CC medicine, and pharmacogenomics. The present sequence is the amino acid  
 CC sequence of the human NOVX28c protein of the invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 7; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60  
 Db |||||  
 QY 1 MECLYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60  
 Db |||||  
 QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
 Db |||||  
 QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
 Db |||||  
 QY 121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180  
 Db |||||  
 QY 121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180  
 Db |||||  
 QY 181 GOYFQKLGRCVRSVSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPIV 240  
 Db |||||  
 QY 181 GOYFQKLGRCVRSVSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPIV 240  
 Db |||||  
 QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLIIHDPSPHFLNYSTINYSKWSFGDNTGLFVSTNHTVN 300  
 Db |||||  
 QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLIIHDPSPHFLNYSTINYSKWSFGDNTGLFVSTNHTVN 300  
 Db |||||  
 QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIIDENCQIN 360  
 Db |||||  
 QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIIDENCQIN 360  
 Db |||||  
 QY 361 RYGHFQATITIVEGILEVNIQMTDVLMPVWPESLIDFVVTQGSIPTEVCTIISDPT 420  
 Db |||||  
 QY 361 RYGHFQATITIVEGILEVNIQMTDVLMPVWPESLIDFVVTQGSIPTEVCTIISDPT 420  
 Db |||||  
 QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTISVPRDRPAS 480  
 Db |||||  
 QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTISVPRDRPAS 480  
 Db |||||  
 QY 481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAV 540  
 Db |||||  
 QY 481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAV 540  
 Db |||||  
 QY 541 FPGNQEKDPLLNQNEFKGVS 560  
 Db |||||  
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 Db |||||

RESULT 11

ADH36879

ID ADH36879 standard; protein; 560 AA.

XX

AC ADH36879;

XX

DT 11-MAR-2004 (first entry)

XX

DE Human lung cancer-related protein #16.

XX

KW lung cancer; lung tumour; immune response stimulation;

XX

KW tumour protein specific T cell; human.

XX

OS Homo sapiens.

XX

PN WO2003086175-A2.

XX

PD 23-OCT-2003.

XX

PF 07-APR-2003; 2003WO-US010945.

XX

PR 05-APR-2002; 2002US-00117982.

PR

PR 04-DEC-2002; 2002US-00313986.

XX

PA (CORI-) CORIXA CORP.

XX

XX Mericle B, Fanger GR, Vedwick TS, Carter D, Watanabe Y;

PI

PI Henderson RA, Kalos MD, Spies GA, Foy TM, Fan L, Wang T, Mcnabb A;

PI

PI Reed SG;

XX

XX WPI; 2003-845247/78.

DR

XX Use of compositions comprising lung tumor polypeptides or

PT

PT polynucleotides, for inhibiting lung cancer or tumor progression,

PT

PT stimulating immune response, or stimulating and/or expanding T cells

PT

XX specific for a tumor protein.

XX

PS Disclosure; SEQ ID NO 225; 456pp; English.

XX

CC The invention comprises a method for inhibiting the development of lung

CC

CC cancer, the method involves the use of compositions which contain lung

CC

CC tumor polypeptides/polynucleotides. The methods and compositions of the

CC

CC invention are useful for inhibiting lung cancer development and tumor

CC

CC progression, stimulating immune response, or stimulating and/or expanding

CC

CC T cells specific for a tumor protein. The present amino acid sequence

CC

XX represents a human lung cancer-related protein.

XX

QY Sequence 560 AA;

QY

Query Match 100.0%; Score 3026; DB 7; Length 560;

QY

Best Local Similarity 100.0%; Pred. No. 4.7e-262;

QY

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

QY 1 MECLYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60

Db

1 MECLYFLGFLLLAARLPDAAKPHDVLGNRPSPAYMEHNLQNGSSDENDWNEKLYP 60

Db

61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120

QY

61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120

Db

121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180

QY

121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHHNVFPDGKPPHGWRRWNIYVFTL 180

Db

181 GOYFQKLGRCVRSVSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPIV 240

QY

181 GOYFQKLGRCVRSVSVNTANVTILGPQLMEVTVYRRHGRAYVPIAQVKDYVVTDOIPIV 240

Db

241 TMFQKNDNRSSDETFLKDLPIFMDVLIIHDPSPHFLNYSTINYSKWSFGDNTGLFVSTNHTVN 300

QY

241 TMFQKNDNRSSDETFLKDLPIFMDVLIIHDPSPHFLNYSTINYSKWSFGDNTGLFVSTNHTVN 300

Db

301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIIDENCQIN 360

QY

301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIIDENCQIN 360

Db

361 RYGHFQATITIVEGILEVNIQMTDVLMPVWPESLIDFVVTQGSIPTEVCTIISDPT 420

QY

361 RYGHFQATITIVEGILEVNIQMTDVLMPVWPESLIDFVVTQGSIPTEVCTIISDPT 420

Db

421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTISVPRDRPAS 480

QY

421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSLTISVPRDRPAS 480

Db

481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAV 540

QY

481 PLRMANSALISVGCCLAIPTVTISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAV 540

Db

541 FPGNQEKDPLLNQNEFKGVS 560

QY

541 FPGNQEKDPLLNQNEFKGVS 560

Db

RESULT 12  
 ID ADJ68660 standard; protein; 560 AA.  
 AC ADJ68660;  
 DT 06-MAY-2004 (first entry)  
 DE Human heat mitochondrial protein as a therapeutic target SegID466.  
 XX mitochondrial; human; screening assay; diabetes mellitus;  
 KW Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHON;  
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteopathic; ophthalmological; cytostatic.  
 OS Homo sapiens.  
 XX  
 PN WO2003087768-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 04-APR-2003; 2003WO-US010870.  
 XX  
 PR 12-APR-2002; 2002US-0372843P.  
 PR 17-JUN-2002; 2002US-0389987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 XX  
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 PI Warnock DE;  
 XX  
 DR WPI; 2003-845369/78.  
 XX  
 PT Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function,  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 XX  
 XX Claim 1; SEQ ID NO 466; 180pp; English.  
 PS  
 PS This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nontropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.  
 XX  
 XX Sequence 560 AA;  
 SQ  
 Query Match 100.0%; Score 3026; DB 7; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-262;  
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MECLLYPLGFLLLAARPLDAAKFDHVLGNRPSAYMRHNLQNGWSSDNDWNEKLYP 60  
 DB 1 MECLLYPLGFLLLAARPLDAAKFDHVLGNRPSAYMRHNLQNGWSSDNDWNEKLYP 60

QY 61 VKRGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120  
 DB 61 VKRGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120  
 QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHPGRRWNFIYVFHTL 180  
 DB 121 RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHPGRRWNFIYVFHTL 180  
 QY 181 GQYFQKLGRCRSVRVSVNTANVTGLPOLMEVTVYRRHGRAYVPIAQVKDVVVTDOI.PVFV 240  
 DB 181 GQYFQKLGRCRSVRVSVNTANVTGLPOLMEVTVYRRHGRAYVPIAQVKDVVVTDOI.PVFV 240  
 QY 241 TMFQKNDNRNSDETEFLKDLPIIMFDVLIHDPSEFLNYSTINYKWSFGDNTGLFVSTNHTVN 300  
 DB 241 TMFQKNDNRNSDETEFLKDLPIIMFDVLIHDPSEFLNYSTINYKWSFGDNTGLFVSTNHTVN 300  
 QY 301 HTYVLNGTFSMLTVKAAAPGCPPPPPPPRRPSKPTPSLGPAGDNPLELSRIPDENCOIN 360  
 DB 301 HTYVLNGTFSMLTVKAAAPGCPPPPPPPRRPSKPTPSLGPAGDNPLELSRIPDENCOIN 360  
 QY 361 RYGHFQATITIVEGILEVNIIOQTDVLMVPWPPESSLIDFVVTGCGSIPTEVCTIISDPT 420  
 DB 361 RYGHFQATITIVEGILEVNIIOQTDVLMVPWPPESSLIDFVVTGCGSIPTEVCTIISDPT 420  
 QY 421 CEITQNTVCGSPVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSLALTSTLISVPDRDPAS 480  
 DB 421 CEITQNTVCGSPVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSLALTSTLISVPDRDPAS 480  
 QY 481 PLRMANSALISVGCIAIFVTVISLIVYKHKYNIENSPGNVRSKGLSVFLNRAKAYF 540  
 DB 481 PLRMANSALISVGCIAIFVTVISLIVYKHKYNIENSPGNVRSKGLSVFLNRAKAYF 540  
 QY 541 FPGNOEKDPLLNQRFKGV 560  
 DB 541 FPGNOEKDPLLNQRFKGV 560  
 RESULT 13  
 ADL14995  
 ID ADL14995 standard; protein; 560 AA.  
 XX ADL14995;  
 AC ADL14995;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Human NMB protein for cancer treatment.  
 XX  
 KW cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;  
 KW prognosis; mantle cell lymphoma; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003068269-A2.  
 XX  
 PD 21-AUG-2003.  
 XX  
 PF 13-FEB-2003; 2003WO-EP001461.  
 XX  
 PR 14-FEB-2002; 2002GB-00003480.  
 PR 29-JUN-2002; 2002GB-00015095.  
 XX  
 PA (BIOI-) BIOINVENT INT AB.  
 XX  
 PI Ek S, Borrebaeck CAK, Ehinger M;  
 XX  
 DR WPI; 2003-697496/66.  
 DR N-PSDB; ADL14995.  
 XX  
 PT New compound for treating, imaging, diagnosing or prognosing mantle cell  
 PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a  
 PT protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.  
 PT nucleic acid).  
 XX

PS Disclosure; SEQ ID NO 7; 342pp; English.

XX The invention relates to a compound comprising a binding moiety which selectively binds to a protein or polypeptide listed in the specification (e.g. human autotaxin polypeptide or human CD24 signal transducer polypeptide), and a further moiety. The compound is useful in medicine or in the treatment, imaging, diagnosis or prognosis of mantle cell lymphomas (MCL). It is used in preparing a medicament for treating MCL, a diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells in the body of an individual. This sequence corresponds to one of the polypeptides of the invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 7; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.7e-262;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60  
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60

QY 61 VMKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120  
DB 61 VMKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120

QY 121 RNEAGLSADPYNNWTAWESDGGTQSHHNVFPDQKPPHHPGWRWNFIYVFHTL 180  
DB 121 RNEAGLSADPYNNWTAWESDGGTQSHHNVFPDQKPPHHPGWRWNFIYVFHTL 180

QY 181 GOYFQKLGRCVRSVNTANVTLGQLMVEVYRRHGRAYVPIAQVKDVIYVTDQIPVF 240  
DB 181 GOYFQKLGRCVRSVNTANVTLGQLMVEVYRRHGRAYVPIAQVKDVIYVTDQIPVF 240

QY 241 TWFQKNDNSDETFLKDLPIWFDVLIHDPHFYLYSTINYKWSFGDNTGLFVSTNHTVN 300  
DB 241 TWFQKNDNSDETFLKDLPIWFDVLIHDPHFYLYSTINYKWSFGDNTGLFVSTNHTVN 300

QY 301 HTYVLNGTFSNLTLVKAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIPDENCQIN 360  
DB 301 HTYVLNGTFSNLTLVKAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIPDENCQIN 360

QY 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSLDIFVTCQGSIPTEVCTIISDPT 420  
DB 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPESSLDIFVTCQGSIPTEVCTIISDPT 420

QY 421 CEITQNTVCSVDVDEMCLLTVRFTFNGSGTYCVNLTGLDDTSLALTSLISVPDRPAS 480  
DB 421 CEITQNTVCSVDVDEMCLLTVRFTFNGSGTYCVNLTGLDDTSLALTSLISVPDRPAS 480

QY 481 PLRMANSALISVGCIAIFVTYISLLVYKKHKEYNPENSPGNVRSKGLSVFLNRAKAVF 540  
DB 481 PLRMANSALISVGCIAIFVTYISLLVYKKHKEYNPENSPGNVRSKGLSVFLNRAKAVF 540

QY 541 PFGNQEKDPLLNQEFKGVG 560  
DB 541 PFGNQEKDPLLNQEFKGVG 560

RESULT 14  
ADN39940  
ID ADN39940 standard; protein; 560 AA.  
XX  
AC ADN39940;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C310.  
XX  
KW Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularisation syndrome; scarring; uterine fibroid;

KW detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnery; gene therapy; vaccine.

XX Homo sapiens.

PN WO2003042661-A2.

XX 22-MAY-2003.

XX 13-NOV-2002; 2002WO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

PR 21-NOV-2001; 2001US-0332464P.

PR 29-NOV-2001; 2001US-0334393P.

PR 03-DEC-2001; 2001US-0335393P.

PR 14-DEC-2001; 2001US-0340376P.

PR 08-JAN-2002; 2002US-0347211P.

PR 10-JAN-2002; 2002US-0347343P.

PR 08-FEB-2002; 2002US-0355250P.

PR 13-FEB-2002; 2002US-0356714P.

PR 20-FEB-2002; 2002US-0359077P.

PR 29-MAR-2002; 2002US-0368809P.

PR 04-APR-2002; 2002US-0370110P.

PR 12-APR-2002; 2002US-0372246P.

PR 05-JUN-2002; 2002US-0386614P.

PR 16-JUL-2002; 2002US-0396839P.

PR 22-JUL-2002; 2002US-0397755P.

PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX WPI: 2003-469649/44.  
XX N-PSDB; ADN39723.

PT Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C310; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularisation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.

XX Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 7; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.7e-262;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60  
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGWSSDENDWNEKLYP 60

QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNTTFAVNLIPRCCKEDANGNIYVEKNC 120  
 DB 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNTTFAVNLIPRCCKEDANGNIYVEKNC 120  
 QY 121 RNEAGLSADPYVYNTAWSEDSGNGTGQSHNVFPDGGKPPHPPGWRWNFIYVFHTL 180  
 DB 121 RNEAGLSADPYVYNTAWSEDSGNGTGQSHNVFPDGGKPPHPPGWRWNFIYVFHTL 180  
 QY 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVYVTDQIPVFV 240  
 DB 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVYVTDQIPVFV 240  
 QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPESHFLNYSTINYKWSGDNGLFVSTNHTVN 300  
 DB 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPESHFLNYSTINYKWSGDNGLFVSTNHTVN 300  
 QY 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360  
 DB 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360  
 QY 361 RYGHFOATITIVEGILEVNIIOQTDVLMVPWPPESSLIIDFVVTCCQSIPTEVCTIISDPT 420  
 DB 361 RYGHFOATITIVEGILEVNIIOQTDVLMVPWPPESSLIIDFVVTCCQSIPTEVCTIISDPT 420  
 QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
 DB 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
 QY 481 PLRMANSLISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVF 540  
 DB 481 PLRMANSLISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVF 540  
 QY 541 FPGNQEKDPLLKNQEPKGVNS 560  
 DB 541 FPGNQEKDPLLKNQEPKGVNS 560

RESULT 15  
 ADH56342  
 ID ADH56342 standard; protein; 560 AA.

AC ADH56342;  
 DT 25-MAR-2004 (first entry)  
 XX Human nmb protein SEQ ID NO:1.  
 DE respiratory disease; human; nmb; antiinflammatory; antiasthmatic;  
 KW antiallergic; neuroprotective; immunosuppressive; antidiabetic;  
 KW antiarthritic; dermatological; gastrointestinal; antirheumatic; asthma;  
 KW hayfever; chronic bronchitis; chronic obstructive lung disease;  
 KW immune disorder; multiple sclerosis; Sjogren's disease;  
 KW insulin-resistant diabetes; rheumatoid arthritis; lupus erythematosus;  
 KW atopic dermatitis; irritable bowel disease.  
 XX Homo sapiens.  
 OS WO2004002516-A1.  
 XX 08-JAN-2004.  
 XX 27-JUN-2003; 2003WO-JP008168.  
 XX 28-JUN-2002; 2002JP-00190790.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX Nakanishi A, Iwashita H, Morita S, Matsumoto T, Yamasaki M;  
 WPI; 2004-082883/08.  
 DR N-PSDB; ADH56343.  
 XX Drug compositions containing inhibitor of human nmb protein activity for

PT treatment and prevention of respiratory diseases including asthma and  
 PT chronic obstructive lung disease.  
 XX Claim 1; SEQ ID NO 1; 104pp; Japanese.  
 CC The present invention describes drug compositions (I) for prevention and  
 CC treatment of respiratory diseases, which contain a compound or its salts  
 CC inhibiting the activity of human nmb protein or its partial peptides or a  
 CC protein of substantially similar sequence and activity, or inhibiting the  
 CC expression of the gene encoding this protein. Also described: (1)  
 CC antisense polynucleotides to all or part of the nmb gene, and drug  
 CC compositions containing them; (2) antibodies to all or part of nmb  
 CC protein, and drug compositions and diagnostic reagents containing them;  
 CC (3) diagnostic reagents containing polynucleotides encoding all or part  
 CC of nmb protein; (4) screening method for compounds for use in prevention  
 CC and treatment of respiratory diseases, using nmb protein or its partial  
 CC peptides, or using polynucleotides encoding all or part of nmb protein,  
 CC or using a tobacco smoking induced chronic obstructive lung disease model  
 CC mouse or an elastase-induced chronic obstructive lung disease model mouse  
 CC; (5) kits for the screening method; (6) compounds identified by the  
 CC screening method; (7) a method for prevention and treatment of  
 CC respiratory diseases using the identified compounds; and (8) drug  
 CC compositions for prevention and treatment of respiratory diseases  
 CC containing a compound or its salts inhibiting the binding activity of  
 CC heparan sulfate proteoglycan. (I) have antiinflammatory, antiasthmatic,  
 CC antiallergic, neuroprotective, immunosuppressive, antidiabetic,  
 CC antiarthritic, dermatological, gastrointestinal, and antirheumatic  
 CC activities. (I) can be used for the prevention, treatment and diagnosis  
 CC of respiratory diseases such as acute asthma, chronic asthma, hayfever,  
 CC chronic bronchitis and chronic obstructive lung disease, and other  
 CC diseases including immune disorders such as multiple sclerosis, Sjogren's  
 CC disease, insulin-resistant diabetes, rheumatoid arthritis, lupus  
 CC erythematosus, atopic dermatitis, and irritable bowel disease. The  
 CC present sequence represents human nmb, which is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 560 AA;

Query Match 100.0%; Score 3026; DB 8; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-262;  
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 1 MECLYYFLGLLLAARLPDAAKRFHDLGNRPSPAYMRHNLQNGWSDENDWNEKLYP 60  
 QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNTTFAVNLIPRCCKEDANGNIYVEKNC 120  
 DB 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNTTFAVNLIPRCCKEDANGNIYVEKNC 120  
 QY 121 RNEAGLSADPYVYNTAWSEDSGNGTGQSHNVFPDGGKPPHPPGWRWNFIYVFHTL 180  
 DB 121 RNEAGLSADPYVYNTAWSEDSGNGTGQSHNVFPDGGKPPHPPGWRWNFIYVFHTL 180  
 QY 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVYVTDQIPVFV 240  
 DB 181 GOYFQKLGRCVRSVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDVYVTDQIPVFV 240  
 QY 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPESHFLNYSTINYKWSGDNGLFVSTNHTVN 300  
 DB 241 TMFQKNDNRSSDETFLKDLPIFMDVLIHDPESHFLNYSTINYKWSGDNGLFVSTNHTVN 300  
 QY 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360  
 DB 301 HTYVLNGTFSNLITVKAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCQIN 360  
 QY 361 RYGHFOATITIVEGILEVNIIOQTDVLMVPWPPESSLIIDFVVTCCQSIPTEVCTIISDPT 420  
 DB 361 RYGHFOATITIVEGILEVNIIOQTDVLMVPWPPESSLIIDFVVTCCQSIPTEVCTIISDPT 420  
 QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480  
 DB 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVPDRDPAS 480

QY	481	PLRMANGALISVGCIAIFVTWISLLVYKHKEYNP	IENSPGNVRSKGLSVFLNRAKVF	540
Db	481	PLRMANGALISVGCIAIFVTWISLLVYKHKEYNP	IENSPGNVRSKGLSVFLNRAKVF	540
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Job time : 164 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 14:59:13 ; Search time 147 Seconds  
(without alignments)  
1349.057 Million cell updates/sec

Title: US-09-853-880A-17  
Perfect score: 3026  
Sequence: 1 MECLYFLGLLAARLPD.....PFGNQKDPKLNQFKGVS 560

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3026	100.0	560	9	US-09-735-705-225
2	3026	100.0	560	9	US-09-850-716A-225
3	3026	100.0	560	9	US-09-897-778-225
4	3026	100.0	560	9	US-09-943-075A-6
5	3026	100.0	560	13	US-10-039-272-2
6	3026	100.0	560	14	US-10-007-700-225
7	3026	100.0	560	14	US-10-117-982-225
8	3026	100.0	560	14	US-10-463-106-2
9	3026	100.0	560	14	US-10-295-027-1258
10	3026	100.0	560	14	US-10-313-986-225
11	3026	100.0	560	15	US-10-309-290-152
12	3026	100.0	560	16	US-10-408-765A-466
13	3006	99.3	572	14	US-10-227-884-42

14	3006	99.3	572	14	US-10-230-163-42	Sequence 42, Appl
15	3006	99.3	572	14	US-10-230-338-42	Sequence 42, Appl
16	3006	99.3	572	14	US-10-218-631-42	Sequence 42, Appl
17	3006	99.3	572	14	US-10-230-414-42	Sequence 42, Appl
18	3006	99.3	572	14	US-10-232-224-42	Sequence 42, Appl
19	3006	99.3	572	14	US-10-216-159A-42	Sequence 42, Appl
20	3006	99.3	572	14	US-10-218-849-42	Sequence 42, Appl
21	3006	99.3	572	14	US-10-227-873-42	Sequence 42, Appl
22	3006	99.3	572	14	US-10-227-883-42	Sequence 42, Appl
23	3006	99.3	572	14	US-10-219-076-42	Sequence 42, Appl
24	3006	99.3	572	14	US-10-230-434-42	Sequence 42, Appl
25	3006	99.3	572	14	US-10-219-003-42	Sequence 42, Appl
26	3006	99.3	572	14	US-10-219-075-42	Sequence 42, Appl
27	3006	99.3	572	14	US-10-219-464-42	Sequence 42, Appl
28	3006	99.3	572	14	US-10-219-466-42	Sequence 42, Appl
29	3006	99.3	572	14	US-10-219-479-42	Sequence 42, Appl
30	3006	99.3	572	14	US-10-219-481-42	Sequence 42, Appl
31	3006	99.3	572	14	US-10-230-260-42	Sequence 42, Appl
32	3006	99.3	572	14	US-10-232-231-42	Sequence 42, Appl
33	3006	99.3	572	14	US-10-232-233-42	Sequence 42, Appl
34	3006	99.3	572	14	US-10-216-165-42	Sequence 42, Appl
35	3006	99.3	572	14	US-10-218-956-42	Sequence 42, Appl
36	3006	99.3	572	14	US-10-219-468-42	Sequence 42, Appl
37	3006	99.3	572	14	US-10-219-478-42	Sequence 42, Appl
38	3006	99.3	572	14	US-10-219-536-42	Sequence 42, Appl
39	3006	99.3	572	14	US-10-233-205-42	Sequence 42, Appl
40	3006	99.3	572	14	US-10-219-072-42	Sequence 42, Appl
41	3006	99.3	572	14	US-10-219-470-42	Sequence 42, Appl
42	3006	99.3	572	14	US-10-219-474-42	Sequence 42, Appl
43	3006	99.3	572	14	US-10-219-524-42	Sequence 42, Appl
44	3006	99.3	572	14	US-10-219-528-42	Sequence 42, Appl
45	3006	99.3	572	14	US-10-227-880-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-09-735-705-225

; Sequence 225, Application US/09735705

; Patent No. US20020052329A1

; GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kalos, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 225

LENGTH: 560

TYPE: PRT

ORGANISM: Homo sapien

US-09-735-705-225

Query Match 100.0%; Score 3026; DB 9; Length 560;

Best Local Similarity 100.0%; Pred. No. 3.6e-245;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYFLGLLAARLPDAAKRFHDVIGNRPSPAYMEHNLQNCWSSDNDWNEKLYP 60





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Db 121 RNEAGLSADPVYVNTWTAWSEDSGNGTQSHNVFPDCKPRPHPGWRRWNFIYVFHTL 180
Qy 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
Qy 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Qy 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Db 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Qy 361 RYGHFOATITIVGILEVNIQMTDVLMPVPPESSLDIVVTCQSGIPTVECTIISDPT 420
Db 361 RYGHFOATITIVGILEVNIQMTDVLMPVPPESSLDIVVTCQSGIPTVECTIISDPT 420
Qy 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPRDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPRDRPAS 480
Qy 481 PLRMANSLISVGCCLAIFFTIVISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSLISVGCCLAIFFTIVISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Qy 541 PFGNOEKDPLLNKQEFKGS 560
Db 541 PFGNOEKDPLLNKQEFKGS 560

RESULT 4
US-09-943-075A-6
; Sequence 6, Application US/09943075A
; Patent No. US20020151486A1
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Faye F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
; FILE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Human
US-09-943-075A-6

Query Match 100.0%; Score 3026; DB 9; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECLYYFLGFLLLAARLPDAAKRFHDVGNERPSPAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVGNERPSPAYMRHNLQNGWSSDENDWNEKLYP 60
Qy 61 VKKGDNRWKNWSKGGVQAVLTSDSPALVGSNTITFAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKKGDNRWKNWSKGGVQAVLTSDSPALVGSNTITFAVNLIFPRCKEDANGNIVYEKNC 120
Qy 121 RNEAGLSADPVYVNTWTAWSEDSGNGTQSHNVFPDCKPRPHPGWRRWNFIYVFHTL 180
Db 121 RNEAGLSADPVYVNTWTAWSEDSGNGTQSHNVFPDCKPRPHPGWRRWNFIYVFHTL 180
Qy 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
Qy 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Qy 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Db 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Qy 361 RYGHFOATITIVGILEVNIQMTDVLMPVPPESSLDIVVTCQSGIPTVECTIISDPT 420
Db 361 RYGHFOATITIVGILEVNIQMTDVLMPVPPESSLDIVVTCQSGIPTVECTIISDPT 420
Qy 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPRDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPRDRPAS 480
Qy 481 PLRMANSLISVGCCLAIFFTIVISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSLISVGCCLAIFFTIVISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Qy 541 PFGNOEKDPLLNKQEFKGS 560
Db 541 PFGNOEKDPLLNKQEFKGS 560
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Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
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Db 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Qy 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Db 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Qy 361 RYGHFOATITIVGILEVNIQMTDVLMPVPPESSLDIVVTCQSGIPTVECTIISDPT 420
Db 361 RYGHFOATITIVGILEVNIQMTDVLMPVPPESSLDIVVTCQSGIPTVECTIISDPT 420
Qy 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPRDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLALTSTLISVPRDRPAS 480
Qy 481 PLRMANSLISVGCCLAIFFTIVISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSLISVGCCLAIFFTIVISLLVYKHKHEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Qy 541 PFGNOEKDPLLNKQEFKGS 560
Db 541 PFGNOEKDPLLNKQEFKGS 560

RESULT 5
US-10-039-272-2
; Sequence 2, Application US/10039272
; Publication No. US20020168653A1
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey
; CURRENT APPLICATION NUMBER: US/10/039,272
; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-272-2

Query Match 100.0%; Score 3026; DB 13; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECLYYFLGFLLLAARLPDAAKRFHDVGNERPSPAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVGNERPSPAYMRHNLQNGWSSDENDWNEKLYP 60
Qy 61 VKKGDNRWKNWSKGGVQAVLTSDSPALVGSNTITFAVNLIFPRCKEDANGNIVYEKNC 120
Db 61 VKKGDNRWKNWSKGGVQAVLTSDSPALVGSNTITFAVNLIFPRCKEDANGNIVYEKNC 120
Qy 121 RNEAGLSADPVYVNTWTAWSEDSGNGTQSHNVFPDCKPRPHPGWRRWNFIYVFHTL 180
Db 121 RNEAGLSADPVYVNTWTAWSEDSGNGTQSHNVFPDCKPRPHPGWRRWNFIYVFHTL 180
Qy 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
Db 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDYVVTQDIPVFV 240
Qy 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Db 241 TMFQKNDNRSSDETFKDLPIMFVDLIHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
Qy 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
Db 301 HTYVLNGTSLNLTVAAPGCPDPPTSPKPTPSLGPAGDNPLESRIIPDENCQIN 360
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Db 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIPDENCQIN 360
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Db 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTCQGSIPTEVCTIISDPT 420
QY 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLSISVPRDRPAS 480
Db 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLSISVPRDRPAS 480
QY 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
QY 541 PFGNQEKDPLLNQBFKGV 560
Db 541 PFGNQEKDPLLNQBFKGV 560

RESULT 6
US-10-007-700-225
; Sequence 225, Application US/10007700
; Publication No. US20030064947A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Foy, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C17
; CURRENT APPLICATION NUMBER: US/10/007,700
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-700-225

Query Match 100.0%; Score 3026; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCQKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCQKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHNVFPDGPFPHPGWRWNFIYVPHTL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHNVFPDGPFPHPGWRWNFIYVPHTL 180
QY 181 GOYFQKLGRCRSVRVSVNTANVTLPQLMEVTVYRRHGRVPIAQVKDVVVTDDIPIVFV 240
Db 181 GOYFQKLGRCRSVRVSVNTANVTLPQLMEVTVYRRHGRVPIAQVKDVVVTDDIPIVFV 240
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QY 241 TMEQKNDRSSDETFLKDLPIMFVDVLIHDPHFNLNYSTINKWSPGDNLTGLFVSTNHTVN 300
Db 241 TMEQKNDRSSDETFLKDLPIMFVDVLIHDPHFNLNYSTINKWSPGDNLTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIPDENCQIN 360
Db 301 HTYVLNGTFSNLTVKAAAGPCPPPPRPSKPTSLGPAGDNPLELSRIPDENCQIN 360
QY 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTCQGSIPTEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIIOQMTDVLMPVPMPSSLIDFVVTCQGSIPTEVCTIISDPT 420
QY 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLSISVPRDRPAS 480
Db 421 CEITQNTVCSFVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLALTSTLSISVPRDRPAS 480
QY 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
Db 481 PLRMANSALISVGCCLAFVTVISLLVYKHKYENPIENSPGNVRSKGLSVFLNRAKAVF 540
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Db 541 PFGNQEKDPLLNQBFKGV 560

RESULT 7
US-10-117-982-225
; Sequence 225, Application US/10117982
; Publication No. US20030138438A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Mericle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-225

Query Match 100.0%; Score 3026; DB 14; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
Db 1 MECLYYFLGLLLAARLPDAAKRFHDVLGNRPSAYMRHNLQNGWSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCQKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIFRCQKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHNVFPDGPFPHPGWRWNFIYVPHTL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTGQSHNVFPDGPFPHPGWRWNFIYVPHTL 180
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Db 181 GOYFQKLGRCVRSVNTANVTILGPQLMVEVTVYRRHGRAYVPIAQVKDVVVVTDQIPVFV 240  
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Db 241 TMFQKNDNRSSDTEFLKDLPIMFQVLIHDPHSFLNVTSTINYKWSFGDNTGLFVSTNHTVN 300  
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Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360  
QY 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420  
Db 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420  
QY 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLDGDDTSLATSTLISVPDRDPAS 480  
Db 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLDGDDTSLATSTLISVPDRDPAS 480  
QY 481 PURMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PURMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540  
QY 541 PFGNOEKDPLLNQBFKGV 560  
Db 541 PFGNOEKDPLLNQBFKGV 560

RESULT 8  
US-10-463-106-2  
; Sequence 2, Application US/10463106  
; Publication No. US20030202938A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMESHWAR, Pranela  
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-1 GENE  
; FILE REFERENCE: 267/033 University of Medicine & Dentistry of New Jersey  
; CURRENT APPLICATION NUMBER: US/10/463,106  
; CURRENT FILING DATE: 2003-06-17  
; PRIOR FILING DATE: 2001-10-20  
; PRIOR APPLICATION NUMBER: US 10/039,272  
; PRIOR FILING DATE: 2001-10-20  
; PRIOR APPLICATION NUMBER: US 60/241,881  
; PRIOR FILING DATE: 2000-10-20  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-463-106-2

Query Match 100.0%; Score 3026; DB 14; Length 560;  
Best Local Similarity 100.0%; Pred. No. 3.6e-245;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYIFLGLFLLAARLPDAAKRFHDLGNRPISAYMREHNQNLGWSDDNDWNEKLYP 60  
Db 1 MECLYIFLGLFLLAARLPDAAKRFHDLGNRPISAYMREHNQNLGWSDDNDWNEKLYP 60  
QY 61 VWKRGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
Db 61 VWKRGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
QY 121 RNEAGLSADPVYVNTAWSESDGNGTGQSHNVFDPGKPPHHPGWRWNFIYVHTL 180  
Db 121 RNEAGLSADPVYVNTAWSESDGNGTGQSHNVFDPGKPPHHPGWRWNFIYVHTL 180  
QY 181 GOYFQKLGRCVRSVNTANVTILGPQLMVEVTVYRRHGRAYVPIAQVKDVVVVTDQIPVFV 240  
Db 181 GOYFQKLGRCVRSVNTANVTILGPQLMVEVTVYRRHGRAYVPIAQVKDVVVVTDQIPVFV 240  
QY 241 TMFQKNDNRSSDTEFLKDLPIMFQVLIHDPHSFLNVTSTINYKWSFGDNTGLFVSTNHTVN 300  
Db 241 TMFQKNDNRSSDTEFLKDLPIMFQVLIHDPHSFLNVTSTINYKWSFGDNTGLFVSTNHTVN 300

QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360  
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPFLSRIIPDENCQIN 360  
QY 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420  
Db 361 RYGHFOATITIVEGILEVNIIOMTDVLMPVPWPESSLIIDFVVTCCQSIPTVEVCTIIISDPT 420  
QY 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLDGDDTSLATSTLISVPDRDPAS 480  
Db 421 CEITQNTVCSVPDVEDMCLLTVRRTFNGSGTYCVNLTLDGDDTSLATSTLISVPDRDPAS 480  
QY 481 PURMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PURMANSALISVGCLAIFFTIVISLLVYKHKYNIPIENSPGNVRSKGLSVFLNRAKAVF 540  
QY 541 PFGNOEKDPLLNQBFKGV 560  
Db 541 PFGNOEKDPLLNQBFKGV 560

RESULT 9  
US-10-295-027-1258  
; Sequence 1258, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gieh, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; FILE REFERENCE: 018501-012500US  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; PRIOR FILING DATE: 2002-02-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1258  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-027-1258

Query Match 100.0%; Score 3026; DB 14; Length 560;  
Best Local Similarity 100.0%; Pred. No. 3.6e-245;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MECLYYFLGFLLLAARLPDAAKRFHDLVGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
Db	1	MECLYYFLGFLLLAARLPDAAKRFHDLVGNRPSPAYMREHNQNLNGWSSDENDWNEKLYP	60
QY	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIPRCQKEDANGNIYVEKNC	120
Db	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIIPRCQKEDANGNIYVEKNC	120
QY	121	RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVPDGPKEPPHHPGWRMNFIVVFHTL	180
Db	121	RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVPDGPKEPPHHPGWRMNFIVVFHTL	180
QY	181	GOYFQKLGRCSVRVSVNTANVTLGPMLEVTYVRHGRAYVPIAQVKDVVVVTDQIPVFF	240
Db	181	GOYFQKLGRCSVRVSVNTANVTLGPMLEVTYVRHGRAYVPIAQVKDVVVVTDQIPVFF	240
QY	241	TFQKNDNRSSDETFKDLPIFMDVLIHDPSSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN	300
Db	241	TFQKNDNRSSDETFKDLPIFMDVLIHDPSSHFLNYSNTINYKWSFGDNTGLFVSTNHTVN	300
QY	301	HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCOIN	360
Db	301	HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSLGPAGDNPLELSRIPDENCOIN	360
QY	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTFVCTIISDPT	420
Db	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTCCQSIPTFVCTIISDPT	420
QY	421	CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLATSLTSLISVPDRDPAS	480
Db	421	CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGDDTSLATSLTSLISVPDRDPAS	480
QY	481	PLRMANSALISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGKLSVFLNRAKAVF	540
Db	481	PLRMANSALISVGCLAFVTVISLLVYKXKHEYNPIENSPGNVVRSGKLSVFLNRAKAVF	540
QY	541	FPGNQEKDPLLNQNEFKGVS	560
Db	541	FPGNQEKDPLLNQNEFKGVS	560
RESULT 11			
US-10-309-290-152			
; Sequence 152, Application US/10309290			
; Publication No. US20040023241A1			
; GENERAL INFORMATION:			
; APPLICANT: Alsobrook II, John P.			
; APPLICANT: Anderson, David W.			
; APPLICANT: Boldog, Ferenc L.			
; APPLICANT: Burgess, Catherine E.			
; APPLICANT: Chilikuru, Rajeev A.			
; APPLICANT: Edinger, Shlomit R.			
; APPLICANT: Gerlach, Valerie L.			
; APPLICANT: Gorman, Linda			
; APPLICANT: Gould-Rothberg, Bonnie E.			
; APPLICANT: Guo, Xiaojia			
; APPLICANT: Jeffers, Michael E.			
; APPLICANT: Ji, Weizhen			
; APPLICANT: Li, Li			
; APPLICANT: Malvankar, Uriel M.			
; APPLICANT: Miller, Charles E.			
; APPLICANT: Murphy, Ryan			
; APPLICANT: Patturajan, Meera			
; APPLICANT: Peyman, John A.			
; APPLICANT: Rastelli, Luca			
; APPLICANT: Rieger, Daniel K.			
; APPLICANT: Shenoy, Suresh G.			
; APPLICANT: Smithson, Glennda			
; APPLICANT: Starling, Gary			
; APPLICANT: Taupier, Raymond J.			
; APPLICANT: Voss, Edward Z.			
; APPLICANT: Zhong, Haihong			
; APPLICANT: Zhong, Mei			
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH			
; FILE REFERENCE: 21402-502A			
; CURRENT APPLICATION NUMBER: US/10/309,290			
; CURRENT FILING DATE: 2002-12-02			

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; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 152
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-290-152

Query Match      100.0%; Score 3026; DB 15; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MECLYYFLGFLLLAARLPDAAKRPDVLGNRPSPAYMREHNQNLNGWSSDENDMNEKLYP 60
Db      1  MECLYYFLGFLLLAARLPDAAKRPDVLGNRPSPAYMREHNQNLNGWSSDENDMNEKLYP 60

Qy      61  VVKGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120
Db      61  VVKGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120

Qy      121  RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHPGWRNRNFIYVFTL 180
Db      121  RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHPGWRNRNFIYVFTL 180

Qy      181  GQYFQKLGRCRVSVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTQIPVFV 240
Db      181  GQYFQKLGRCRVSVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTQIPVFV 240

Qy      241  TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300
Db      241  TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300

Qy      301  HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGNPLSLRIPDENCIN 360
Db      301  HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGNPLSLRIPDENCIN 360

Qy      361  RYGHFQATITIVGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTVECTIISDPT 420
Db      361  RYGHFQATITIVGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTVECTIISDPT 420

Qy      421  CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVDPDRPAS 480
Db      421  CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVDPDRPAS 480

Qy      481  PLRMANSALISVGCLAIFTVTVISLLVYKKHKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
Db      481  PLRMANSALISVGCLAIFTVTVISLLVYKKHKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540

Qy      541  FPGNQEKDPLLNQOEFGKVS 560
Db      541  FPGNQEKDPLLNQOEFGKVS 560

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RESULT 13  
US-10-227-884-42

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RESULT 12
US-10-408-765A-466
; Sequence 466, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-466

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Query Match      100.0%; Score 3026; DB 16; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.6e-245;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MECLYYFLGFLLLAARLPDAAKRPDVLGNRPSPAYMREHNQNLNGWSSDENDMNEKLYP 60
Db      1  MECLYYFLGFLLLAARLPDAAKRPDVLGNRPSPAYMREHNQNLNGWSSDENDMNEKLYP 60

Qy      61  VVKGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120
Db      61  VVKGDMRWKNSWKGRRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYVEKNC 120

Qy      121  RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHPGWRNRNFIYVFTL 180
Db      121  RNEAGLSADPYVYNWTAWSESDSGENGTCQSHHNVFPDGKPPHPGWRNRNFIYVFTL 180

Qy      181  GQYFQKLGRCRVSVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTQIPVFV 240
Db      181  GQYFQKLGRCRVSVSVNTANVTLPQLMEVTVYRRHGRAYVPIAQVKDQVYVVTQIPVFV 240

Qy      241  TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300
Db      241  TMFQKNDNRNSDETFLKDLPIIMFDVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300

Qy      301  HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGNPLSLRIPDENCIN 360
Db      301  HTYVLNGTFSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGNPLSLRIPDENCIN 360

Qy      361  RYGHFQATITIVGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTVECTIISDPT 420
Db      361  RYGHFQATITIVGILEVNIQMTDVLMPVPWPSSLIIDFVVTQCGSIPTVECTIISDPT 420

Qy      421  CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVDPDRPAS 480
Db      421  CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLGGDTSALTSTLISVDPDRPAS 480

Qy      481  PLRMANSALISVGCLAIFTVTVISLLVYKKHKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540
Db      481  PLRMANSALISVGCLAIFTVTVISLLVYKKHKEYNPIENSPGNVVRSGLSVFLNRAKAVF 540

Qy      541  FPGNQEKDPLLNQOEFGKVS 560
Db      541  FPGNQEKDPLLNQOEFGKVS 560

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Sequence 42, Application US/10227884  
Publication No. US20030027988A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William L.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C79  
CURRENT APPLICATION NUMBER: US/10/227,884  
CURRENT FILING DATE: 2002-08-26  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
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PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
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PRIOR FILING DATE: 1998-12-23  
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PRIOR FILING DATE: 1999-01-12  
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PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733



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,	PRIOR APPLICATION NUMBER:	60/151733



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; PRIORITY FILING DATE: 1999-08-31
; PRIORITY APPLICATION NUMBER: 60/164418
; PRIORITY FILING DATE: 1999-11-09
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; PRIORITY FILING DATE: 1999-12-07
; PRIORITY APPLICATION NUMBER: 60/169495
; PRIORITY FILING DATE: 1999-12-07
; PRIORITY APPLICATION NUMBER: 60/169835

Query Match          99.3%; Score 3006; DB 14; Length 572;
Best Local Similarity 97.7%; Pred. No. 1.8e-243;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGSSDENDWNEKLYP 60
DB 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGSSDENDWNEKLYP 60

61 VVKRGMWKNKSGRQVAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120
DB 61 VVKRGMWKNKSGRQVAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120

121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHNVFPDCKPFPHPGWRWNFIYVFTL 180
DB 121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHNVFPDCKPFPHPGWRWNFIYVFTL 180

181 GOYFQKLGRCVSVVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQIPVFV 240
DB 181 GOYFQKLGRCVSVVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQIPVFV 240

241 TMFQKNDNRSSDETFLKDLPIMFVDLIHDPVSHFLVNSTYINVKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIMFVDLIHDPVSHFLVNSTYINVKWSFGDNTGLFVSTNHTVN 300

301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSL-----GPAGDNPLE 348

349 LSRIPDENCQINRYGHQATITIVEGILEVNIQMTDVLMPVPWPESSLIDFVVTQCGSI 408
DB 361 LSRIPDENCQINRYGHQATITIVEGILEVNIQMTDVLMPVPWPESSLIDFVVTQCGSI 420

409 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCNVLTGDDTSLAITS 468
DB 421 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCNVLTGDDTSLAITS 480

469 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 528
DB 481 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 540

529 LSVFLNRAKAVFFPGNQEKDPLLNQKQEPKGV 560
DB 541 LSVFLNRAKAVFFPGNQEKDPLLNQKQEPKGV 572

RESULT 15
US-10-230-338-42
; Sequence 42, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIORITY APPLICATION NUMBER: 10/119,480
; PRIORITY FILING DATE: 2002-04-09
; PRIORITY APPLICATION NUMBER: 60/059113
; PRIORITY FILING DATE: 1997-09-17
; PRIORITY APPLICATION NUMBER: 60/062287
; PRIORITY FILING DATE: 1997-10-17
; PRIORITY APPLICATION NUMBER: 60/063549
; PRIORITY FILING DATE: 1997-10-28
; PRIORITY APPLICATION NUMBER: 60/064103
; PRIORITY FILING DATE: 1997-10-31
; PRIORITY APPLICATION NUMBER: 60/069873
; PRIORITY FILING DATE: 1997-12-17
; PRIORITY APPLICATION NUMBER: 60/078910
; PRIORITY FILING DATE: 1998-03-20
; PRIORITY APPLICATION NUMBER: 60/079294
; PRIORITY FILING DATE: 1998-03-25
; PRIORITY APPLICATION NUMBER: 60/079656
; PRIORITY FILING DATE: 1998-03-26
; PRIORITY APPLICATION NUMBER: 60/079728
; PRIORITY FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 42
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-230-338-42
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Query Match          99.3%; Score 3006; DB 14; Length 572;
Best Local Similarity 97.7%; Pred. No. 1.8e-243;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGSSDENDWNEKLYP 60
DB 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGSSDENDWNEKLYP 60

61 VVKRGMWKNKSGRQVAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120
DB 61 VVKRGMWKNKSGRQVAVLTSDSPALVGSNITFAVNLIPRCOKEDANGNIYVEKNC 120

121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHNVFPDCKPFPHPGWRWNFIYVFTL 180
DB 121 RNEAGLSADPYVYNNWTAWSESDGNGTGQSHNVFPDCKPFPHPGWRWNFIYVFTL 180

181 GOYFQKLGRCVSVVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQIPVFV 240
DB 181 GOYFQKLGRCVSVVNTANVTLPQMEVTVYRRHGRAYVPIAQVKDYVVTQIPVFV 240

241 TMFQKNDNRSSDETFLKDLPIMFVDLIHDPVSHFLVNSTYINVKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIMFVDLIHDPVSHFLVNSTYINVKWSFGDNTGLFVSTNHTVN 300

301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAGPCPPPPPPRPSKPTPSL-----GPAGDNPLE 348

349 LSRIPDENCQINRYGHQATITIVEGILEVNIQMTDVLMPVPWPESSLIDFVVTQCGSI 408
DB 361 LSRIPDENCQINRYGHQATITIVEGILEVNIQMTDVLMPVPWPESSLIDFVVTQCGSI 420

409 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCNVLTGDDTSLAITS 468
DB 421 PTEVCTIISDPTCEITQNTVCSVDVDMCLLTVRTFNGSGTYCNVLTGDDTSLAITS 480

469 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 528
DB 481 TLISVPDRDPASPLRMANSALISVGCLAFVTVISLLVYKXKEYNPINSPGNVVRSGK 540

529 LSVFLNRAKAVFFPGNQEKDPLLNQKQEPKGV 560
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Db 541 LSVFLNRAKAVFFPGNQERDPLLNQEFKGS 572

Search completed: November 19, 2004, 15:11:31  
Job time : 150 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 14:42:06 ; Search time 199 Seconds  
(without alignments)  
1619.145 Million cell updates/sec

Title: US-09-853-880A-17  
Perfect score: 3026  
Sequence: 1 MECLYFLGLLLAARLPID.....PFGNQKDPLLKNQEPKGVGS 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3026	100.0	560	1	NMB_HUMAN	Q14956 homo sapien
2	3026	100.0	560	2	AAP22336	Aap22336 homo sapi
3	3010	99.5	572	2	Q8N1A1	Q8N1A1 homo sapien
4	3006	99.3	572	2	Q8UUX1	Q8UUX1 homo sapien
5	3006	99.3	572	2	AAQ89481	AAQ89481 homo sapi
6	2197	72.6	574	2	Q8BVV9	Q8BVV9 mus musculu
7	2197	72.6	574	2	Q9QXA0	Q9QXA0 mus musculu
8	2197	72.6	574	2	Q99P91	Q99P91 mus musculu
9	2193	72.5	574	2	Q8BXL4	Q8BXL4 mus musculu
10	2179	72.0	572	2	Q8P7C7	Q8P7C7 rattus norv
11	2179	72.0	572	2	AAH61725	AAH61725 rattus norv
12	2163	71.5	572	2	Q9QZF6	Q9QZF6 rattus norv
13	2042	67.5	526	2	Q8BVA0	Q8BVA0 mus musculu
14	1588.5	52.5	559	1	QNR_COTJA	Q90372 coturnix co
15	1029	34.0	206	2	Q96F58	Q96F58 homo sapien
16	1022	33.8	206	2	Q8IXJ5	Q8IXJ5 homo sapien
17	736.5	24.3	721	2	Q6DDN6	Q6DDN6 xenopus lae
18	729.5	24.1	746	2	Q6DIR2	Q6DIR2 xenopus tro
19	671.5	22.2	626	2	Q9CZB2	Q9CZB2 mus musculu
20	659	21.8	626	1	PM17_MOUSE	Q60696 mus musculu
21	653.5	21.6	760	2	Q6DW64	Q6DW64 gallus gall
22	651	21.5	733	2	Q93391	Q93391 coturnix co
23	651	21.5	733	2	AA82576	AA82576 coturnix
24	650.5	21.5	764	2	Q6DW63	Q6DW63 gallus gall
25	650	21.5	763	2	Q6DW62	Q6DW62 gallus gall
26	642.5	21.2	788	2	Q6DW65	Q6DW65 gallus gall
27	639	21.1	762	1	P115_CHICK	Q98917 gallus gall
28	634	21.0	783	2	Q6DW60	Q6DW60 gallus gall
29	631	20.9	759	2	Q6DW61	Q6DW61 gallus gall
30	622	20.6	661	1	PM17_HUMAN	P40967 homo sapien
31	622	20.6	661	2	AAP35866	AAP35866 homo sapi

32 459 15.2 491 1 PM17\_BOVIN Q06154 bos taurus  
33 399 13.2 461 2 Q97884 O97884 equus cabal  
34 247.5 8.2 236 2 Q9QY67 Q9QY67 mus musculu  
35 182 6.0 397 2 Q8N3R2 Q8N3R2 homo sapien  
36 181.5 6.0 423 2 Q8N0W9 Q8N0W9 homo sapien  
37 181.5 6.0 423 2 AAQ88946 AAQ88946 homo sapi  
38 181 6.0 435 2 Q8N3G9 Q8N3G9 homo sapien  
39 167 5.5 141 2 Q9QY70 Q9QY70 mus musculu  
40 156 5.2 419 2 Q6NXM3 Q6NXM3 mus musculu  
41 155 5.2 419 2 AAH67004 AAH67004 mus muscu  
42 155.5 5.1 354 2 Q8IY46 Q8IY46 homo sapien  
43 144 4.8 3988 2 Q8TPZ1 Q8TPZ1 methanosarc  
44 142.5 4.7 1817 2 Q8TI59 Q8TI59 methanosarc  
45 140 4.6 688 2 Q8TR88 Q8TR88 methanosarc

#### ALIGNMENTS

RESULT 1  
NMB\_HUMAN  
ID NMB\_HUMAN STANDARD; PRT; 560 AA.  
AC Q14956;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Putative transmembrane protein NMB precursor (Transmembrane  
DE Glycoprotein HGFIN).  
GN Name=GNMB; Synonyms=NMB, HGFIN;  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Melanoma;  
RX MEDLINE=95113576; PubMed=7814155;  
RA Weternan M.A.J., Ajubi N., van Dinter I.M.R., Degen W.G.J.,  
RA van Muijen G.N.P., Ruiter D.J., Bloemers H.P.J.;  
RT "NMB, a novel gene, is expressed in low-metastatic human melanoma cell  
RT lines and xenografts.";  
RL Int. J. Cancer 60:73-81(1995).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Peripheral blood;  
RX MEDLINE=22498106; PubMed=12609765;  
RA Bandari P.S., Qian J., Yehia G., Joshi D.D., Maloof P.B., Potian J.,  
RA Oh H.S., Gascon P., Harrison J.S., Rameshwar P.;  
RT "Hematopoietic growth factor inducible neurokinin-1 type: a  
RT transmembrane protein that is similar to neurokinin 1 interacts with  
RT substance P.";  
RL Regul. Pept. 111:169-178(2003).  
CC -!- FUNCTION: Could be a melanogenic enzyme (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- TISSUE SPECIFICITY: Not restricted to the melanocytic lineage.  
CC -!- DEVELOPMENTAL STAGE: Expression in poorly metastatic melanoma cell  
CC lines; no expression in highly metastatic melanoma cell lines.  
CC -!- SIMILARITY: Belongs to the Pmel-17/NMB family.  
CC -!- SIMILARITY: Contains 1 PKD domain.

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EMBL; X76534; CAA54044.1; -.  
DR EMBL; AF322909; AAG42839.1; -.  
DR PIR; I38065; I38065.  
DR Genew; HGNC:4462; GPNMB.  
DR MIM; 604368; -.

DR GO:0016021; C: integral to membrane; TAS.  
DR GO:0008285; P: negative regulation of cell proliferation; TAS.  
DR InterPro: IPR000601; PKD.  
DR Pfam: PF00801; PKD; 1.  
DR PROSITE: PS0093; PKD; 1.  
KW Glycoprotein; Polymorphism; Signal; Transmembrane.  
FT SIGNAL 1 21  
FT CHAIN 22 560  
FT DOMAIN 22 486  
FT TRANSMEM 487 507  
FT DOMAIN 508 560  
FT DOMAIN 240 327  
FT DOMAIN 320 332  
FT CARBOHYD 93 93  
FT CARBOHYD 134 134  
FT CARBOHYD 146 146  
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FT CARBOHYD 249 249  
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FT CARBOHYD 312 312  
FT CARBOHYD 447 447  
FT CARBOHYD 455 455  
FT VARIANT 195 195  
FT VARIANT 197 197  
FT SEQUENCE 560 AA; 62643 MW; 570035B48CCE3ECC CRC64;  
Query Match 100.0%; Score 3026; DB 1; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.5e-218;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 61 VKRGMWKNKSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120  
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DB 121 RNEAGLSADPYVYVNTAWSEDSGNGTQSHNVFPDGPFPFHPCWRWNFIYVFHTL 180  
QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVYVTDQIPVFV 240  
DB 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVYVTDQIPVFV 240  
QY 241 TMFQKNDNRSSDTEFLKDLPIMPDVLIHDPVSHFLNYSNTINYSFGDNTGLFVSTNHTVN 300  
DB 241 TMFQKNDNRSSDTEFLKDLPIMPDVLIHDPVSHFLNYSNTINYSFGDNTGLFVSTNHTVN 300  
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DB 301 HTVYLVNGTFSNLNITVXAAAPCPPPPPPPPPPPPSKPTSLGPNGLSRI PDENCQIN 360  
QY 361 RYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLIIDFVVCQGISPIEVCVTIISDPT 420  
DB 361 RYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLIIDFVVCQGISPIEVCVTIISDPT 420  
QY 421 CEITQNTVCSFVVDENCLLTVTRTFNGSGTYCNVLTGLDDTSLALTSTLISVDPDRPAS 480  
DB 421 CEITQNTVCSFVVDENCLLTVTRTFNGSGTYCNVLTGLDDTSLALTSTLISVDPDRPAS 480  
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DB 481 PLRWANSLISVGCIAIFVTVISLIVYKHKYENPIENSPGVRSKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLNQNEFKGVS 560

DB 541 FPGNQEKDPLLNQNEFKGVS 560  
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AC AAP22336;  
DT 02-NAR-2004 (TREMBlrel. 27, Created)  
DT 02-NAR-2004 (TREMBlrel. 27, Last sequence update)  
DE 02-NAR-2004 (TREMBlrel. 27, Last annotation update)  
DE Hypothetical protein GPNMB.  
GN GPNMB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RX MEDLINE=99063792; PubMed=9847074;  
RA Wilson R.;  
RT "Toward a complete human genome sequence.";  
RL Genome Res. 8:1097-1108(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kalicki J., Kramer J.;  
RT "The sequence of Homo sapiens BAC clone CTA-271G13.";  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Waterston R.H.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
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KW Hypothetical protein.  
SQ SEQUENCE 560 AA; 62643 MW; 570035B48CCE3ECC CRC64;  
Query Match 100.0%; Score 3026; DB 2; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.5e-218;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYYFLGLLLAARLPDAAKRFHDLGNERSAYMRHNLNGWSSDENDWNEKLYP 60  
DB 1 MECLYYFLGLLLAARLPDAAKRFHDLGNERSAYMRHNLNGWSSDENDWNEKLYP 60  
QY 61 VKRGMWKNKSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120  
DB 61 VKRGMWKNKSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCOKEDANGNIVYEKNC 120  
QY 121 RNEAGLSADPYVYVNTAWSEDSGNGTQSHNVFPDGPFPFHPCWRWNFIYVFHTL 180  
DB 121 RNEAGLSADPYVYVNTAWSEDSGNGTQSHNVFPDGPFPFHPCWRWNFIYVFHTL 180  
QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVYVTDQIPVFV 240  
DB 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQKDVVYVTDQIPVFV 240  
QY 241 TMFQKNDNRSSDTEFLKDLPIMPDVLIHDPVSHFLNYSNTINYSFGDNTGLFVSTNHTVN 300

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Db      241 TMFQKNDNRSSDETFLKDLPIIMFDVLIHDPHFNLSTYNYKWSFGDNTGLFVSTNHTVN 300
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Db      301 HTYVLNGTFSNLNLTVAAPGCPPPPPRRSKTSPSLGPDGNDPPLSLSRIPDNCQIN 360
QY      361 RYGHFQATITIVGILEVNIQMTDVLMPVPMPPESSLDIFVVTCCGSIPTVECTIIISOPT 420
Db      361 RYGHFQATITIVGILEVNIQMTDVLMPVPMPPESSLDIFVVTCCGSIPTVECTIIISOPT 420
QY      421 CEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTGLGDDTSLALTSTLISVPRDRPAS 480
Db      421 CEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTGLGDDTSLALTSTLISVPRDRPAS 480
QY      481 PLRMANSALISVGCLAIFFVTISLLVYKHKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
Db      481 PLRMANSALISVGCLAIFFVTISLLVYKHKHKEYNPIENSPGNVRSKGLSVFLNRAKAVF 540
QY      541 FPGNQEKDPLLNQKQEFKGV 560
Db      541 FPGNQEKDPLLNQKQEFKGV 560

RESULT 3
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ID QBNI1A1 PRELIMINARY; PRT; 572 AA.
AC QBNI1A1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GPNMB protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032783; AAH32783.1; -
DR InterPro; IPR000601; PKD.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00093; PKD; 1.
SQ SEQUENCE 572 AA; 63922 MW; 2465C12CF0F3996 CRC64;

Query Match 99.5%; Score 3010; DB 2; Length 572;
Best Local Similarity 97.9%; Pred. No. 4.1e-217;
Matches 560; Conservative 0; Mismatches 0; Indels 12; Gaps 1;

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QY      1 MECLYFFLGFLLLAARLPDAAKRFHDLGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60
Db      1 MECLYFFLGFLLLAARLPDAAKRFHDLGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60
QY      61 VWKRGDMWKSWSKGRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYKNC 120
Db      61 VWKRGDMWKSWSKGRVQAVLTSDSPALVGSNITFAVNLIPPRCKEDANGNIYKNC 120
QY      121 RNEAGLSADPYVYNWTAMSEDSGNGTGQSHNVFPDGKPPHPHGRWRWNFIYVFHTL 180
Db      121 RNEAGLSADPYVYNWTAMSEDSGNGTGQSHNVFPDGKPPHPHGRWRWNFIYVFHTL 180
QY      181 GQYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDQVYVVDQIPVFV 240
Db      181 GQYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDQVYVVDQIPVFV 240
QY      241 TMFQKNDNRSSDETFLKDLPIIMFDVLIHDPHFNLSTYNYKWSFGDNTGLFVSTNHTVN 300
Db      241 TMFQKNDNRSSDETFLKDLPIIMFDVLIHDPHFNLSTYNYKWSFGDNTGLFVSTNHTVN 300
QY      301 HTYVLNGTFSNLNLTVAAPGCPPPPPRRSKTSPSL-----GPAGNDPPL 348
Db      301 HTYVLNGTFSNLNLTVAAPGCPPPPPRRSKTSPSLATLTKSYDNTFGPDGNDPPL 360
QY      349 LSRIPDNCQINRYGHFOATITIVGILEVNIQMTDVLMPVPMPPESSLDIFVVTCCGSI 408
Db      361 LSRIPDNCQINRYGHFOATITIVGILEVNIQMTDVLMPVPMPPESSLDIFVVTCCGSI 420
QY      409 PTEVCTIIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTGLGDDTSLATS 468
Db      421 PTEVCTIIISDPTCEITQNTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTGLGDDTSLATS 480
QY      469 TLISVPRDRPASPLRMANSALISVGCLAIFFVTISLLVYKHKHKEYNPIENSPGNVRSKG 528
Db      481 TLISVPRDRPASPLRMANSALISVGCLAIFFVTISLLVYKHKHKEYNPIENSPGNVRSKG 540
QY      529 LSVFLNRAKAVFFPGNQEKDPLLNQKQEFKGV 560
Db      541 LSVFLNRAKAVFFPGNQEKDPLLNQKQEFKGV 572

RESULT 4
QBUVX1
ID QBUVX1 PRELIMINARY; PRT; 572 AA.
AC QBUVX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NMB.
GN ORFNames=UNQ1725;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RT Genome Res. 13:2265-2270 (2003).
DR EMBL; AY359124; AAQ89481.1; -
DR InterPro; IPR000601; PKD.

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DR SMART; SM00089; PKD; 1.
DR PROSITE; PS0093; PKD; 1.
SQ SEQUENCE 572 AA; 63952 MW; D8C20E0499C018CE CRC64;

Query Match
Best Local Similarity 99.3%; Score 3006; DB 2; Length 572;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNQNLGWSDDNDWNEKLYP 60
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNQNLGWSDDNDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVYKNC 120
DB 61 VKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVYKNC 120
QY 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRWRFIYVFHTL 180
DB 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRWRFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVYVVDQIPV 240
DB 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVYVVDQIPV 240
QY 241 TMFQKNDNRSSDETFLKDLPIPFVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIPFVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
QY 349 LSRIPDENCQINRYGHFQATITIVGILEVNIITQMDVLMVPWPWESSLIDFVTCQSSI 408
DB 349 LSRIPDENCQINRYGHFQATITIVGILEVNIITQMDVLMVPWPWESSLIDFVTCQSSI 408
QY 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
DB 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
QY 421 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 480
DB 421 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 480
QY 469 TLISVDPDRPASPLRMANSALISVGCLAFVTVVISLLVYKKHKEYNPIENSPGNVRSKG 528
DB 469 TLISVDPDRPASPLRMANSALISVGCLAFVTVVISLLVYKKHKEYNPIENSPGNVRSKG 528
QY 529 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 560
DB 529 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 560
QY 541 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 572
DB 541 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 572

RESULT 5
AAQ89481 PRELIMINARY; PRT; 572 AA.
AC AAQ89481;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE NMB.
GN UNQ1725.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

RA Godowski P.;
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY359124; AAQ89481.1; -.
SQ SEQUENCE 572 AA; 63952 MW; D8C20E0499C018CE CRC64;

Query Match
Best Local Similarity 99.3%; Score 3006; DB 2; Length 572;
Matches 559; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNQNLGWSDDNDWNEKLYP 60
DB 1 MECLYFLGFLLLAARLPDAAKRFHDLGNRPSAYMREHNQNLGWSDDNDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVYKNC 120
DB 61 VKRGDMRWKNSWKGSRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVYKNC 120
QY 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRWRFIYVFHTL 180
DB 121 RNEAGLSADPYVYNNWTAMSEDSGNGTQSHHNVFPDGPFPHPGWRWRFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVYVVDQIPV 240
DB 181 GOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHGRAYVPIAQVKDVYVVDQIPV 240
QY 241 TMFQKNDNRSSDETFLKDLPIPFVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMFQKNDNRSSDETFLKDLPIPFVLIHDPHFNLNSTINYKWSFGDNTGLFVSTNHTVN 300
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
DB 301 HTYVLNGTFSNLTVKAAAPGCPPPPPPPRPSKPTPSL-----GPAGDNPLE 348
QY 349 LSRIPDENCQINRYGHFQATITIVGILEVNIITQMDVLMVPWPWESSLIDFVTCQSSI 408
DB 349 LSRIPDENCQINRYGHFQATITIVGILEVNIITQMDVLMVPWPWESSLIDFVTCQSSI 408
QY 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
DB 409 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 468
QY 421 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 480
DB 421 PTEVCTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTLDGDTSLALTS 480
QY 469 TLISVDPDRPASPLRMANSALISVGCLAFVTVVISLLVYKKHKEYNPIENSPGNVRSKG 528
DB 469 TLISVDPDRPASPLRMANSALISVGCLAFVTVVISLLVYKKHKEYNPIENSPGNVRSKG 528
QY 529 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 560
DB 529 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 560
QY 541 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 572
DB 541 LSVFLNRKAVFPFGNQEKDPLLKNQEFKGV 572

RESULT 6
Q8BVV9 PRELIMINARY; PRT; 574 AA.
AC Q8BVV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732452017 product:glycoprotein (transmembrane) nmb,
DE full insert sequence.
GN Name=Gpmmb;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;

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RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang G.M., Heieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA	Whiting J., Helton E., Ketterman M., Madan A., Rodrigues S., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Bradakey A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skaleka U., Smalusz D.E., Schnerch A., Schein J.E.,
RA	Jones S.U., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]	
RP	SEQUENCE FROM N.A.
RC	STRAIN=FVB/N; TISSUE=Salivary gland;
RA	Straussberg R.;
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF322054; AAH14240.1; -;
DR	EMBL; BC026375; AAA26375.1; -;
DR	MCD; MGJ-1934765; Gpmmb.
DR	GO; GO:0005887; C:integral to plasma membrane; IDA.
DR	GO; GO:0008201; F:heparin binding; IDA.
DR	GO; GO:0005178; F:integrin binding; IDA.
DR	GO; GO:0007155; P:cell adhesion; IDA.
DR	InterPro: IPR000583; GATase_2.
DR	InterPro: IPR000601; PKD.
DR	SMART; SMW0089; PKD; 1.
DR	PROSITE; PS00443; GATABSE_TYPE II; UNKNOWN_1.
DR	PROSITE; PSS0093; PKD; 1.
KW	Transmembrane.
SQ	SEQUENCE 574 AA; 63674 MW; B6AE9AC27AB6ACD0 CRC64;

  

Query Match	72.6%; Score 2197; DB 2; Length 574;
Best Local Similarity	70.7%; Pred. No. 3.9e-156;
Matches 403; Conservative	69; Mismatches 82; Indels 16; Gaps 2;

  

QY	1	MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSAYMRHNQLNGWSSDENNDWEKLYP	60
Db	1	MESLCGVLGFLLLAAGLPLQAQRFDVLGHEQYPNHRHNQLRGWSSDENDEHLYP	60
QY	61	VWRKGDMRWKNWSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCQEKEDANGNIYVEKNC	120
Db	61	VVRGDKRWKDSWEGGRVQAVLTSDSPALVGSNITFVVNLVFRCQEKEDANGNIYVEKNC	120
QY	121	RNEAGLSADPVYVNTWTAWSEDSDCENGTSQHSHNVDFDGKPPPHPGWRWNFYLVPHTL	180
Db	121	RNDLGLTSLDLVYVNTWTAGDDGWEDGTSTRSQHLRFDPDRFPFRPHGKKWSFVYVPHTL	180
QY	181	GQYFQKLGRCSRVSIVNTANVTLPQLMWEVTVYRRHGRAWPIAQVKDVVYVTDQIPVFV	240
Db	181	GQYFQKLGRCSARSIVNTNLTAGQPMWEVTVFPRYGAVIPISKVDVYVTDQIPVFV	240
QY	241	TMFQKDNRSSDETFLKDLPIMFDVLIDHPSHFNINYSTINYKWSFGMDNTGLFVSTNNHTVN	300
Db	241	TMSQKNRNLTSDIEFLRDLPVFDVLIDHPSHFLNDSAISYKKNFPGDNTGLFVSNNTLN	300
QY	301	HTYVLINGTFSLNLTKAAAPGPCP-----PPPPPRP-----SKETPSILGPAGD	344
Db	301	HTYVLINGTFNLNLVTQAVPGCPPPSPSTPPPTSPSPSPLFTLUSTPSLUMPTYG	360
QY	345	NPLEISRTPDENCOINRYGHFOATTIVEGILEVNIQTMDVLMPVPMPESLSIDFVVTC	404
Db	361	KSMELDSLNSCNCRINRYGFRAITIVEGILEVISMQIADVPMPTQPANSLMDFVTC	420
QY	405	QGSIPTVECTTIISDPTCEITQNTVCSPVDVDEMCLLTVRRFTNGSGTYCVNLTGDDTSL	464
Db	421	KGATEMEACTIISDPTCOIAONRVCSPVAVDGLCILSVRRAFNMSGTYCVNFTLGDASL	480







```

Db      61  VWRGGRWKDSEGRVQAALTSQSHHNFPPDCKPPHFGWRWNFIVYVHTL 120
      121  RNEAGLSADPYVYNTAWSEDSGNGTQSHHNFPPDCKPPHFGWRWNFIVYVHTL 180
      121  RSDLELASDPYVYNTAWGADDEDWEDSTQGHLPFDGKPPRPHGRKKWNFIVYVHTL 180
      181  GQYFQKLGRCVSRSVNTANVTLPQMEVTVRRHGRAYPIAQKDVYVVTQDQIPFV 240
      181  GQYFQKLGRCVSRSVNTANVTLPQMEVTVRRHGRAYPIAQKDVYVVTQDQIPFV 240
      241  TMFQKNDNRSSDETLKOLPIFEDVLHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
      241  TMVQKNDNRSSDETLKOLPIFEDVLHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
      301  HTYVLNGTFSNLTVKAAAPGCPPPPPTPRP-----SKTPSLGPGADNP 346
      301  HTYVLNGTFSNLTVKAAAPGCPPPPPTPRP-----SKTPSLGPGADNP 346
      347  LELSRIPDENCOINRYGHFOATITVEGILEVNIQMTDVLMPVWPWPESSLDIFVVTGQ 406
      361  MELSDISNENCRINRYGYFRATITVDGILEVNIQVADVPITPQDPSLMDFIYVTCG 420
      407  SIPTVECTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLAL 466
      421  ATPTACTIISDPTCQIAQNRVCSVAVDELCLSVRAFNAGSGTYCVNLTGDDASLAL 480
      467  TSTLSVDRDPASPRLMANSALISVGCLAIPTVTVISLVYKKHKEYNPIENSPGNVRS 526
      481  TSALISIFGKDLGSLRTVNGVLSIGCLAMFVMTVILLYKKHKEYNPIENSPGNVRS 540
      527  KGLSVFLNRAKAVFPFGNCKDPLLNQ 554
      541  KGLSVFLSHAKAFPSRGDREKDLQDK 568

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## RESULT 12

```

ID Q9QZF6 PRELIMINARY; PRT; 572 AA.
AC Q9QZF6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Osteoactivin.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RX MEDLINE=21611396; PubMed=11746512;
RA Safadi F.F., Xu J., Smock S.L., Rico M.C., Owen T.A., Popoff S.N.;
RT "Cloning and characterization of osteoactivin, a novel cDNA expressed
in osteoblasts."
RL J. Cell. Biochem. 84:12-26(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Odgren P.R., Marks S.C. Jr.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Xu J., Safadi F.F., Rosenzweig A.B., Popoff S.N.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184983; AAF03400.1; -.
DR InterPro; IPR000601; PKD.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00093; PKD; 1.
SQ SEQUENCE 572 AA; 63772 MW; CB939F043EC57EB CRC64;

```

## Query Match

```

Best Local Similarity 71.5%; Score 2163; DB 2; Length 572;
Matches 394; Conservative 75; Mismatches 85; Indels 14; Gaps 1;

```

```

QY      1  MECLYYFLGLLLAARLPDAAKPRHDVILGNRPSPAYMREHNQNLNGSSDENWNEKLYP 60
      1  MESLCGLVFLLLAAGLPQAAKPRFDVLGHEQYPDHRENNQLRCWSSDENWDEQLYP 60
      61  VMKRGDMRWKNSWKGGRVQAALTSQSHHNFPPDCKPPHFGWRWNFIVYVHTL 120
      61  VMRGEGRWKDSEGRVQAALTSQSHHNFPPDCKPPHFGWRWNFIVYVHTL 120
      121  RNEAGLSADPYVYNTAWSEDSGNGTQSHHNFPPDCKPPHFGWRWNFIVYVHTL 180
      121  RSDLELASDPYVYNTAWGADDEDWEDSTQGHLPFDGKPPRPHGRKKWNFIVYVHTL 180
      181  GQYFQKLGRCVSRSVNTANVTLPQMEVTVRRHGRAYPIAQKDVYVVTQDQIPFV 240
      181  GQYFQKLGRCVSRSVNTANVTLPQMEVTVRRHGRAYPIAQKDVYVVTQDQIPFV 240
      241  TMFQKNDNRSSDETLKOLPIFEDVLHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
      241  TMVQKNDNRSSDETLKOLPIFEDVLHDPSPHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
      301  HTYVLNGTFSNLTVKAAAPGCPPPPPTPRP-----SKTPSLGPGADNP 346
      301  HTYVLNGTFSNLTVKAAAPGCPPPPPTPRP-----SKTPSLGPGADNP 346
      347  LELSRIPDENCOINRYGHFOATITVEGILEVNIQMTDVLMPVWPWPESSLDIFVVTGQ 406
      361  MELSDISNENCRINRYGYFRATITVDGILEVNIQVADVPITPQDPSLMDFIYVTCG 420
      407  SIPTVECTIISDPTCEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGDDTSLAL 466
      421  ATPTACTIISDPTCQIAQNRVCSVAVDELCLSVRAFNAGSGTYCVNLTGDDASLAL 480
      467  TSTLSVDRDPASPRLMANSALISVGCLAIPTVTVISLVYKKHKEYNPIENSPGNVRS 526
      481  TSALISIFGKDLGSLRTVNGVLSIGCLAMFVMTVILLYKKHKEYNPIENSPGNVRS 540
      527  KGLSVFLNRAKAVFPFGNCKDPLLNQ 554
      541  KGLSVFLSHAKAFPSRGDREKDLQDK 568

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## RESULT 13

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Q8BVA0 PRELIMINARY; PRT; 526 AA.
ID Q8BVA0;
AC Q8BVA0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Mus musculus adult male urinary bladder cDNA, RIKEN full-length
enriched library, clone:953038P20 product:glycoprotein
DE (transmembrane) nmb, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RL MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RL MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RA The FANTOM Consortium,

```



FT DOMAIN 23 487 Extracellular (Potential).  
FT TRANSMEM 488 508 Potential.  
FT DOMAIN 509 559 Cytoplasmic (Potential).  
FT DOMAIN 239 326 PKD.  
FT CARBOHYD 92 92 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 133 133 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 145 145 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 149 149 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 192 192 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 199 199 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 248 248 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 274 274 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 307 307 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 311 311 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 459 459 N-linked (GlcNAc. . .) (Potential).  
SQ SEQUENCE 559 AA; 61713 MW; 81E2793BD6447DD CRC64;  
  
Query Match 52.5%; Score 1588.5; DB 1; Length 559;  
Best Local Similarity 53.5%; Pred. No. 1.7e-110;  
Matches 297; Conservative 86; Mismatches 157; Indels 15; Gaps 5;  
  
QY 8 LGFILLARLPDAKRFHVLGNERPSAYMREHNQNGSWSDNDWNEKLYPVWKRGM 67  
Db 8 LALLPAEAVLCAAAARFQDVLNAGR-TAPVTNHHKIQGWSDDQNKNEKLYPFWEEDNDP 66  
  
QY 68 RWKNSWKGQVAVLTSDSPALVGSNITPAVNLIIPRCOKEDANGNIYVKKCRNEAGLS 127  
Db 67 RKWDCWKGKVTKLVTUSPALVGSNITPAVNLIIPRCOKEDDGNIIYQRNCTPDSPA 126  
  
QY 128 ADPVYNNWTAMSESDSGENGTCQSHHNVFPDGPFPHPGMRMNFIVFHTLQGYFOKL 187  
Db 127 QDQVYNNTEWIDNCGWENCTSNHSHNVFPDGPFPHPGMRMNFIVFHTLQGYFOKL 186  
  
QY 188 GRCSRVSVNTANTVLTGQLEVTYRRHGRAYVPIAQKOVYVTDQIPVFTVMFQKND 247  
Db 187 GRSSANFSVNTANTVLTGQLEVTYRRHGRAYVPIAQKOVYVTDQIPVFTVMFQKND 246  
  
QY 248 RNSDDETLKDLPIEMFDVLIHDPSEFLAVSTINYKWSFGDNTGLFVSTNHTVHTVYVNG 307  
Db 247 RNSDDETLKDLPIEMFDVLIHDPSEFLAVSTINYKWSFGDNTGLFVSTNHTVHTVYVNG 306  
  
QY 308 TFSNLMTVKAAPGCPPPPPPPRPSKPTPSL-----GPGNDPLSLKIPDENCQI 359  
Db 307 NFTNLMTVKAAPGCPPPPPPPRPSKPTPSL-----GPGNDPLSLKIPDENCQI 363  
  
QY 360 NRYGHFQATITIVGILEVNIQMTDVLMPVWPVPESSLIDFVVTQGSIPTEVCTIISDP 419  
Db 364 YRYGYTATITIVGILEVNIQMTDVLMPVWPVPESSLIDFVVTQGSIPTEVCTIISDP 423  
  
QY 420 TCEITQNTVCSVDVDENCLLTVRRTEGSGTYCVNLTLGDDTSLALSTLISVPDRDPA 479  
Db 424 TCQVSGQWCVDPVVDENCLLTVRRTEGSGTYCVNLTLGDDTSLALSTLISVPDRDPA 480  
  
QY 480 SPLRMANSLISVGLAIFVTIVISLLVYKHKEYNPIENSPGNVRSKGLSVFLNRAKAV 539  
Db 481 SSSGTTKGVFIFLGLAVGAIGAFVLYKRYKQYKPIERSAGQENQGLSAYVSNFKAF 540  
  
QY 540 FPGNQEKDPLKNO 554  
Db 541 FFPKSTERNPLKSK 555

RESULT 15

Q96F58 PRELIMINARY; PRT; 206 AA.  
AC Q96F58  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein GPNMB (Glycoprotein (Transmembrane) nmb).  
GN Name=GPNMB;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skin;  
RX Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Kainine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
RA Phelan M., Farmer A.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99063792; PubMed=9847074;  
RA Wilson R.;  
RT "Toward a complete human genome sequence.";  
RL Genome Res. 8:1097-1108 (1998).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Kalicki J., Kramer J.;  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RA Waterston R.H.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
RN [8]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A.  
RA Waterston R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011595; AAH11595.1; -  
DR EMBL; BT007074; AAP35737.1; -  
DR EMBL; AC005082; AAP22337.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
KW Hypothetical protein; Transmembrane.  
SQ SEQUENCE 206 AA; 23945 MW; 30CBDE6928D73FBD CRC64;

Query Match	34.0%;	Score 1029;	DB 2;	Length 206;
Best Local Similarity	98.4%;	Pred. No. 4.2e-69;		
Matches 182;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MECLYFLGELLAAARLPDAAKRFHFDVGNRPSAYMREHNQNLGWSDDENDWNEKLYP	60	
Db	1	MECLYFLGELLAAARLPDAAKRFHFDVGNRPSAYMREHNQNLGWSDDENDWNEKLYP	60	
Qy	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCQEDANGNIYVEKNC	120	
Db	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFFRCQEDANGNIYVEKNC	120	
Qy	121	RNEAGLSADPYYVNTWTAWSDDSGENTGQSHNVFPDGKFPFPHPGWRWNFIYVVFHTL	180	
Db	121	RNEAGLSADPYYVNTWTAWSDDSGENTGQSHNVFPDGKFPFPHPGWRWNFIYVVFHTL	180	
Qy	181	GQVFQ	185	
Db	181	GWLLQ	185	

Search completed: November 19, 2004, 14:59:05  
Job time : 202 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 14:50:11 ; Search time 41 Seconds  
(without alignments)  
134.180 Million cell updates/sec

Title: US-09-853-880A-17

Perfect score: 3026

Sequence: 1 MECLYFLGLAARLPD.....PFGNQKDPLLKNQBFKGV 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3026	100.0	560	2 I38065	gene NMB protein - human
2	659	21.8	626	2 S53871	Pmei 17 protein -
3	622.5	20.6	662	2 I38400	melanoma-associate
4	617.5	20.4	668	2 A41234	melanocyte-specific
5	459	15.2	491	2 A49179	melanoma antigen h
6	136	4.5	926	1 A41105	protein-tyrosine-p
7	120.5	4.0	446	2 T07907	hydroxyproline-tic
8	114.5	3.8	1009	2 C64483	hypothetical prote
9	111.5	3.7	457	2 I55976	dihydroliipoamide S
10	111.5	3.7	555	2 S21766	hypothetical membr
11	109.5	3.6	348	2 AB3260	TipC protein - sli
12	108	3.6	3848	2 T17414	hypothetical prote
13	106.5	3.5	848	2 T23694	genome polyprotein
14	106	3.5	1874	1 J00533	protein F21D18.18
15	105	3.5	492	2 C96521	probable periplasm
16	104.5	3.5	363	2 G83306	transforming prote
17	104.5	3.5	624	1 I51581	surface proteinase
18	104.5	3.5	837	2 C69200	polycystic kidney
19	104.5	3.5	840	2 B69216	hypothetical prote
20	104.5	3.5	4302	2 A38971	ATP-dependent DNA
21	104	3.4	913	2 T18503	retinoblastoma pro
22	102.5	3.4	674	2 A10922	regulatory factor
23	102.5	3.4	921	2 A33718	hypothetical prote
24	102.5	3.4	979	2 A35913	hypothetical prote
25	101.5	3.4	445	2 D81716	hypothetical prote
26	101	3.3	588	2 T45564	hypothetical prote
27	101	3.3	705	2 T16088	hypothetical prote
28	101	3.3	2014	2 T21560	hypothetical prote
29	100.5	3.3	221	2 T07176	extensin homolog -

## ALIGNMENTS

### RESULT 1

I38065

gene NMB protein - human

C:Species: Homo sapiens (man)

C>Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004

C:Accession: I38065

R:Weterman, M.A.; Ajubi, N.; van Dinter, I.M.; Degen, W.G.; van Muijen, G.N.; Ruitter, Int. J. Cancer 60, 73-81, 1995

A:Title: nmb, a novel gene, is expressed in low-metastatic human melanoma cell lines an

A:Reference number: I38085; MUID:95113576; PMID:7814155

A:Accession: I38065

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-560 <RES>

A:Cross-references: UNIPROT:Q14956; EMBL:X76534; NID:g666042; PIDN:CAA54044.1; PID:g666

C:Genetics:

A:Gene: GDB:NMB

A:Cross-references: GDB:I20237; OMIM:162340

A:Map position: 15q22-15qter

Query Match	100.0%;	Score 3026;	DB 2;	Length 560;
Best Local Similarity	100.0%;	Pred. No. 3e-227;		
Matches 560;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MECLYVFLGLLLAARLPDAAKRFHDVLGNERSAYMREHNLQNGWSSDENDWNEKLYP	60	
Db	1	MECLYVFLGLLLAARLPDAAKRFHDVLGNERSAYMREHNLQNGWSSDENDWNEKLYP	60	
QY	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC	120	
Db	61	VWKGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIVYEKNC	120	
QY	121	RNEAGLSADPVYVNTAWSDSGENGTSQSHNVFPDGKPPHPHQRWRNFIVYFHTL	180	
Db	121	RNEAGLSADPVYVNTAWSDSGENGTSQSHNVFPDGKPPHPHQRWRNFIVYFHTL	180	
QY	181	GOYFQKLGRCRSVRVSVNTANVTLGPQLMEVTVVRRHGRAYVPIAOVKDVVVVTDQIPVFV	240	
Db	181	GOYFQKLGRCRSVRVSVNTANVTLGPQLMEVTVVRRHGRAYVPIAOVKDVVVVTDQIPVFV	240	
QY	241	TMFQKNDNRNSDDETFKDLPIMFVDLHDPSEFLNXTINYKWSFGDNTGLFVSTNHTVN	300	
Db	241	TMFQKNDNRNSDDETFKDLPIMFVDLHDPSEFLNXTINYKWSFGDNTGLFVSTNHTVN	300	
QY	301	HTYVLNGTFSNLTVKAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIDENQCIN	360	
Db	301	HTYVLNGTFSNLTVKAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIDENQCIN	360	
QY	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTTCQGSIPTEVCTIISDPT	420	
Db	361	RYGHFOATITIVEGILEVNIQMTDVLMPVPWPPESSLIDFVVTTCQGSIPTEVCTIISDPT	420	

twitching motility  
hypothetical prote  
lin-1 protein - Ca  
hypothetical prote  
botulinum neurotox  
hypothetical prote  
titin, cardiac mus  
hypothetical prote  
receptor tyrosine  
receptor tyrosine  
hypothetical prote  
platelet-derived g  
ATP-dependent DNA  
hypothetical prote  
hypothetical prote  
hypothetical prote

QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTTCVNLTLGGDTSLATSTLISVPRDPAAS 480  
DB 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTTCVNLTLGGDTSLATSTLISVPRDPAAS 480  
QY 481 PLRMANSLISVGCCLAFVTVLSLLVYKXKHEYNPIENSGNVRSKGLSVFLNRAKAVF 540  
DB 481 PLRMANSLISVGCCLAFVTVLSLLVYKXKHEYNPIENSGNVRSKGLSVFLNRAKAVF 540  
QY 541 PFGNQEKDPLLNQKQFKGVS 560  
DB 541 PFGNQEKDPLLNQKQFKGVS 560  
RESULT 2  
Pmel 17 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S53871  
R:Kwon, B.S.; Halaban, R.; Ponnazhagan, S.; Kim, K.; Chintamaneni, C.; Bennett, D.; Pick  
Nucleic Acids Res. 23, 154-158, 1995  
A:Title: Mouse silver mutation is caused by a single base insertion in the putative cyto  
A:Reference number: S53871; MUID:95175358; PMID:7870580  
A:Accession: S53871  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-626 <KWO>  
A:Cross-references: UNIPROT:Q60696; GB:U14133; NID:g887940; PIDN:AAA69538.1; PID:g887941

Query Match 21.8%; Score 659; DB 2; Length 626;  
Best Local Similarity 27.2%; Pred. No. 3.5e-43;  
Matches 183; Conservative 99; Mismatches 211; Indels 180; Gaps 20;  
QY 7 FLGFLLLAARLPDA--AKRFHDLGNRPSAYMREHNLQNGWSSDENDWNEKLYPVWKR 64  
DB 9 FLPLVLALLAVGALSGRNQDLGVPRQV-----TKTWNRLQLYPEWT- 53  
QY 65 GDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIVVEKN-CRNE 123  
DB 54 -EVQGSNCWRGQVSLRVINDGPTLVGANASFIALHFFGQSKVLDPDQGVWANNTIING 112  
QY 124 AGLSADPYVYNWTAWSEDSGNGTCQSHNVFPDCKPRPHHPGMRNFIYFHTLGOY 183  
DB 113 SQVWGQPVTP-----QEPDQA-----CVFPGGCPDGPCKPRKPSFYVWKTWGKY 159  
QY 184 FQKLGRCVRSVNTANVTILGPOLMEVTVYRRHG-RAYVPIAQVKDQVYVTDQIPVFVTM 242  
DB 160 WQVLGGPVSRSSATRAHKLGTHTMEVTVYHRRGQSQYVPLAHASSTFTTIDQVPFSVS 219  
QY 243 FQKDRNSDDETLKDLPIPMFDVLIHDPHFLNYSINIKWSFGDNTGLFVSTNHTVNT 302  
DB 220 SQLQALDGETKHLRNLPLIFALQLHDPGSLAEADLSYTWDFDGTGLTISRALDVTHT 279  
QY 303 YVLNGTFLNLTAKA-----APGP 322  
DB 280 YLSSGVSVAQVLOALPLVSCSSPVPGTTDGYMTABAPTTSRQITTKVGTGTPGQ 339  
QY 323 CPPPPP-----PPRPS-----K 334  
DB 340 MPTTPQSGTWTWQMTTEVATTSEQMLTSAVIDTTLAEVSTTEGTGTTTRPSGTVAQ 399  
QY 335 PPSLGPAGNPL-----ELSRPDE-----NCQINRYGHFOATITVE 373  
DB 400 ATTEGPDGA-SPLLPQTSGTSISPLDDTDTIMLVKRVPLDCLVLYRGSFSLALDIVQ 458  
QY 374 GILEVNIQMTDVLMPVPWPPESSLIDFVWTCQSGSIPTVECTIISDPTCEITQNTVCSVD 433  
DB 459 G-----IESAEILQAVPFSEGDFAELTVSCQGLPKEACMDISSPCQPPAQLCQSV 512  
QY 434 VDEMCLLTVRRTF-NGSGTTCVNLTLGGDTSLATSTLISVPRDPAASPLRMANSLISV 492  
DB 513 PSPDCQLVHLQVLKGGSGTTCVNLVSLADANSLAVASTQLVVPDQDGG-----LQAPLLV 567

QY 493 GCLAFVTVI--SLIV---YKKHKEYN-----PIENSGNVRSKGLSVFLNRAKAVFP 542  
DB 568 GLLLVIVAVLWLASLTLDLSRAQFPKCHMVLTAAASGLRARGLG----- 615  
QY 543 GNOEKDPLLNQKQ 555  
DB 616 ---ENSPILSGQ 625  
RESULT 3  
I38400  
melanoma-associated ME20 antigen (me20m) - human  
N:Alternate names: melanoma antigen 25  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: I38400; A53668; A55753  
R:Marresh, G.A.; Marken, J.S.; Neubauer, M.; Aruffo, A.; Hellstrom, I.; Hellstrom, K.;  
DNA Cell Biol. 13, 87-95, 1994  
A:Title: Cloning and expression of the gene for the Melanoma-Associated ME20 Antigen.  
A:Reference number: I38400; MUID:94235165; PMID:8179825  
A:Accession: I38400  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-662 <RES>  
A:Cross-references: UNIPROT:P40967; EMBL:U01874; NID:G494939; PIDN:AAA18479.1; PID:G494939  
R:Adema, G.J.; de Boer, A.J.; Vogel, A.M.; Loenen, W.A.M.; Figdor, C.G.  
J. Biol. Chem. 269, 20126-20133, 1994  
A:Title: Molecular characterization of the melanocyte lineage-specific antigen gp100.  
A:Reference number: A53668; MUID:94327568; PMID:7519602  
A:Accession: A53668  
A:Molecule type: mRNA  
A:Residues: 1-592,594-662 <ADE>  
A:Cross-references: GB:S73003; NID:G639589; PIDN:AAC60634.1; PID:G639590  
R:Kawakami, Y.; Elyahu, S.; Delgado, C.H.; Robbins, P.F.; Sakaguchi, K.; Appella, E.;  
Proc. Natl. Acad. Sci. U.S.A. 91, 6458-6462, 1994  
A:Title: Identification of a human melanoma antigen recognized by tumor-infiltrating ly  
A:Reference number: A55753; MUID:94294401; PMID:8022805  
A:Accession: A55753  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-161,'F',163-592,594-662 <XAW>  
C:Keywords: glycoprotein

Query Match 20.6%; Score 622.5; DB 2; Length 662;  
Best Local Similarity 25.5%; Pred. No. 2.6e-40;  
Matches 168; Conservative 93; Mismatches 199; Indels 199; Gaps 17;  
QY 3 CLYYFLGFLLLAARLPDAK--RFHDLGNRPSAYMREHNLQNGWSSDENDWNEKLYP 60  
DB 8 CL---LHLAVIGALLAVGATKVPNRQDLGVSR-----QLR-----TKAWNRLQLYP 50  
QY 61 VMKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIVVEKN 120  
DB 51 EWT--BAORLDCWRGQVSLKLVNDGPTLVGANASFIALNFPFGSKVLDPDQGVVWNT 108  
QY 121 RNEAGLSADPYVN---W---TAWSEDSGNGTCQSHNVFPDCKPRPHHPGMRNFIYFHTLGOY 173  
DB 109 -----INGQVWGQPVYFQETDDA-----CIFDGGCPDGPCKPRKPSFYVWKTWGKY 149  
QY 174 IYVFHTLGOYFQKLGRCVRSVNTANVTILGPOLMEVTVYRRHG-RAYVPIAQVKDQVYV 232  
DB 150 VYVWKWQVQVGLGPGVSGLSIGTGRAMLGTHTMEVTVYHRRGSRSYVPLAHSSAFTI 209  
QY 233 TDQIPVFVTMFOKDRNSDDETLKDLPIPMFDVLIHDPHFLNYSINIKWSFGDNTGLF 292  
DB 210 TDQVPFSVSQVLRALDGGNKHLRNLPLIFALQLHDPGSLAEADLSYTWDFDGSSTGL 269  
QY 293 VSTNHTVNTYVNLNGTFLNLTAKAAP-----GPCPPP----- 327  
DB 270 ISRALVVTHTYLFEPGPVTAQVLOALPLTSCSSPVPGTTDGHRTAEAPNTTAGOVPT 329  
QY 328 ----- 327



Db 330 TEVVGTTGQAPTAEPSGTTTQVPTTEVISTAPVQMPTAESTGMTPEKVPSEVMGTTL 389  
QY 328 -----PPRPSKP----- 335  
Db 390 AEMSTPEATGMTPAEVSIVLGGTTAAQVTTTEWVETARELPPEPEGPDASSIMSTES 449  
QY 336 -TPSLGPAGDNPLELSRIPE---NCQINRYGHFQATITIVEGILEVNIQMTDVLMPVP 391  
Db 450 ITGSLGPLDGTATLRLVKRQVPLDCVLYRGSFVTLDIVQ-----IESAEILQAVP 503  
QY 392 WPESLIDFVTCQSGIPTEVCTIISDPTCEITQNTVCSFVDVDEMCLLTVRRTF-NGSG 450  
Db 504 SGEQDAFELTVSCQGLPKAEKWEISSPGCQPAQRLCQVLPSPACQLVLHQLKGGSG 563  
QY 451 TYCVNLTGLDGTSLATSLTSLISVDRDPASPLRMANSALISVGCCLAFVTVI-SLL 505  
Db 564 TYCLNVSLADTNSLAVVSTQLIMP--VPGILLTQGEAGLGQVPLIVGILLVLMVAVLASL 621  
QY 506 VYKK 509  
Db 622 IYRR 625

RESULT 4  
A41234  
melanocyte-specific protein Pmel-17 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 30-Sep-1993  
C:Accession: A41234  
R:Kwon, B.S.; Chintamaneni, C.; Kozak, C.A.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.;  
Proc. Natl. Acad. Sci. U.S.A. 88, 9228-9232, 1991  
A:Title: A melanocyte-specific gene, Pmel 17, maps near the silver coat color locus on m  
A:Reference number: A41234; MUID:92021023; PMID:1924386  
A:Accession: A41234  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-668 <KWO>  
A:Cross-references: GB:M77348

Query Match 20.4%; Score 617.5; DB 2; Length 668;  
Best Local Similarity 25.8%; Pred. No. 6.4e-40;  
Matches 171; Conservative 93; Mismatches 197; Indels 203; Gaps 19;

QY 3 CLYFLGFLLLAARLPDAAK--RPHDVLGNRPSPAYMRHNLQNGWSSDENDMNEKLYP 60  
Db 8 CL--LHLAVTGALLAVGATKVPKQDNLGYSR-----QLR-----TKAMNRQLYP 50

QY 61 VWKGRDMRWKSKGGRQAVLTSDSPALVGSNITFAVNLIFPRCKEDANGNIYVEKNC 120  
Db 51 EWT--EAQRLDCWGGQVSLKVSNDGPTLIGANASFSIALNFPQSKVLPDQGVTVWNT 108

QY 121 RNEAGLSADPVYN---W---TAWSESDGNGTGQSHHNVFPDQKFPFPHPGWRRWNF 173  
Db 109 -----IINGSQVWGGQVVPVQETDDA-----CIFPDGQPCSSGSKHSF 149

QY 174 IYVFTLQYFQKLGRCVRSVNTANVTLPQMEVTVYRRHG-RAVVPQAQKDVVYV 232  
Db 150 VYVWKTQYVQVLLGGVPSGLSIGTRAMLTHTMEVTVYHRRGSRVYVLAHSSAFTI 209

QY 233 TDQIPVFVTFQKNDNRSSDFTFLKDLPIFMDVLIHDPESHFNSTINYKWSFGDNGCLF 292  
Db 210 TDQVPFVSVSQALRDGNGKHFLENQDLTALQLHDPSCGYLAELSYTDFDGSSTGL 269

QY 293 VSTNHTVNTVLTNGTFSNLITVKAAP-----GPCPPPP----- 327  
Db 270 ISRAPVTVHTYLEPGVTAQVVLQAAIPLTSCGSSPVPGTTDGHRTAEAPNTAGQVPT 329

QY 328 ----- 327

Db 330 TEVVGTTGQAPTAEPSGTTTQVPTTEVISTAPVQMPTAESTGMTPEKVPSEVMGTTL 389

QY 328 -----PPRPSKP----- 335

Db 390 AEMSTPEATGMTPAEVSIVLGGTTAAQVTTTEWVETARELPPEPEGPDASSIMSTES 449

QY 336 -TPSLGPAGDNPLELSRIPE---NCQINRYGHFQATITIVEGILEVNIQMTDVLMPVP 391

Db 450 ITGSLGPLDGTATLRLVKRQVPLDCVLYRGSFVTLDIVQ-----IESAEILQAVP 503  
QY 392 WPESLIDFVTCQSGIPTEVCTIISDPTCEITQNTVCSFVDVDEMCLLTVRRTF-NGSG 450  
Db 504 SGEQDAFELTVSCQGLPKAEKWEISSPGCQPAQRLCQVLPSPACQLVLHQLKGGSG 563  
QY 451 TYCVNLTGLDGTSLATSLTSLISVDRDPASPLRMANSALISVGCCLAFVTVI-SLL 505  
Db 564 TYCLNVSLADTNSLAVVSTQLIMP--VPGILLTQGEAGLGQVPLIVGILLVLMVAVLASL 621  
QY 506 VYKK 509  
Db 622 IYRR 625

RESULT 5  
A49179  
melanoma antigen homolog rpe1 - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A49179; I45861  
R:Kim, R.Y.; Wistow, G.J.  
Exp. Eye Res. 55, 657-662, 1992  
A:Title: The cDNA RPE1 and monoclonal antibody HMB-50 define gene products preferential  
A:Reference number: A49179; MUID:93122163; PMID:1478275  
A:Accession: A49179  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-491 <KIM>  
A:Cross-references: UNIPROT:Q06154  
A:Experimental source: retinal pigment epithelium  
A:Note: sequence extracted from NCBI backbone (NCBIN:122438, NCBI:122439)  
C:Genetics:  
A:Gene: RPE1

Query Match 15.2%; Score 459; DB 2; Length 491;  
Best Local Similarity 26.6%; Pred. No. 8.7e-28;  
Matches 122; Conservative 64; Mismatches 130; Indels 142; Gaps 12;

QY 182 QYFQKLGRCVRSVNTANVTLPQMEVTVYRRHG-RAVVPQAQKDVVTVVTDQIPVFPV 240  
Db 1 QYQVVLGSPVSLGSLGTDKAMLTGYNMEVTVYHRRGSSQSYVPLAHSSAFTITDQVPFSV 60

QY 241 TMFQKNDNRSSDFTFLKDLPIFMDVLIHDPESHFNSTINYKWSFGDNGTGLFVSTNHTVN 300  
Db 61 SVSOLQALDGRNKRFLRKQPLTFALQLHDPSCGYLAGADLSYTWDFDGTGLISRALVT 120

QY 301 HTYVLNGTFSNLITVKAAP---GPCPPPPPPPP----- 331  
Db 121 HTYLESGPVTAQVVLQAAIPLTSCGSPFPVPGTTDRHVTAEAPGTTAGQVPTTEVMGTT 180

QY 332 ----- 333

Db 181 GOVPTAEAPGTTVGVPTTEDVGTTPQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPS 240

QY 334 KPTPSLG-----PAGDN-----PLE-----LSRIPDE----- 355

Db 241 GTTVTQGTTPBELVETAGEVSTPEPAGSNTSSFPTEGTAGSLSPLEDDTATLVLEKQA 300

QY 356 --NCQINRYGHFQATITIVEGILEVNIQMTDVLMPVPPESSLIIDFVTCQSGIPTEVC 413  
Db 301 PLDCVLYRGSFSLTDLVS-----IESAEILQAVSSGSEGAFAFELTVSCQGLPKAEAC 353

QY 414 TIISDPTCEITQNTVCSFVDVDEMCLLTVRRTF-NGSGTYCVNLTGLDGTSLATSLTSLIS 472  
Db 354 MDLSSPCQIPQRLCQVPPSPACQLVLHQLKGGSGTYCLNVSLADNSLAVVSTQLV 413

QY 473 VPRDRDPASPLRMANSALISVGCCLAFVTVI-SLLVYKK 509  
Db 414 MPQGE--AGLRQAP---LFGVILLVLTALLASLIYRR 446

RESULT 6

A41105  
protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human  
N:Alternate names: PTPase (MAN)  
C:Species: Homo sapiens (man)  
C:Date: 20-Mar-1992 #sequence\_revision 02-May-1994 #text\_change 09-Jul-2004  
C:Accession: A41105  
R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.  
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991  
A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty  
A:Reference number: A41105; MUID:91288564; PMID:1648233  
A:Accession: A41105  
A:Molecule type: mRNA  
A:Residues: 1-926 <GUA>  
A:CROSS-references: UNIPROT:P29074; GB:M68941; NID:G190747; PIDN:AAA36530.1; PID:G190748  
A:Experimental source: megakaryocytes, cell line MEG-10  
C:Genetics:  
A:Gene: GDB:PTPN4  
A:CROSS-references: GDB:131387; OMIM:176878  
A:Map position: 9q31-9q31  
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; P  
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas  
F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>  
F:523-597/Domain: GLGF domain homology <GLG>  
F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>  
F:852/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:858/Binding site: substrate phosphate (Arg) #status predicted

Query Match 4.5%; Score 136; DB 1; Length 926;  
Best Local Similarity 22.0%; Pred. No. 0.027;  
Matches 87; Conservative 43; Mismatches 125; Indels 140; Gaps 17;  
QY 40 EHNQLN-----GWSNDWNEKLYPVWGRDMRWKNSWKGGRVQAVLTSDSP 87  
DB 204 EFNLTARTLELYGVEFYHARDQSN-NEIMIGWMSGGILLYKN-----RVRNMTFP 254  
QY 88 ALVGSNITFVNLIFPCCKEDANG-----NIVVEKCRNEAGLSADPVYVNWTAWE 140  
DB 255 WLKIVISFKCKOFFIQRLKELHSEKTLGFGNWNVYRACKN-----LWKACVE 303  
QY 141 DSDGNGTGGSHNVDPGKPPFPHPGRWRNFIYFHTLGYQFKLGRCSV-----192  
DB 304 -----HHTFRLDRLFPQK-----NFFAHYFTLGSFKFRYCGRTEVQSVGYKE 347  
QY 193 -----RVSVNTANVTGLQPMLEVTVRRHGRVPIAQKDVVVVTDQIPVFTMQKND 247  
DB 348 KANKDRVFARSPSKPLARKLMDWEVSRN-----SISDDRLETQSLPSRPPGTPNH 399  
QY 248 RNSG-----DETFLKDLPI--MFDVLIH-DPSH-FLNYSNTINKWSFGDNTGLFVSTNHTVN 300  
DB 400 RNSTFTQEGTRLRPSVGHVLVDHVTSPSEVFNQR-----SPSSTQA 443  
QY 301 HTYVLNGTFLSLNLTVAAPGCPGPPPPPP-----331  
DB 444 NSIVLESSPS-----QETPDGKPPALPPQSKNSWNQIYHSHSQDLESHINETFDI 497  
QY 332 ---PSKPTPSLGPAGNPLESRIPDENCCINRYG 363  
DB 498 PSSPEKPTPGGIPHDNLVIRMKPDEN---GRFG 529

RESULT 7  
T07907  
hydroxyproline-rich glycoprotein GAS28 precursor - Chlamydomonas reinhardtii  
C:Species: Chlamydomonas reinhardtii  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C:Accession: T07907  
R:Rodriguez-Martinez, H.; Haring, M.A.; Von Gromof, E.; Beck, C.F.  
submitted to the EMBL Data Library, July 1997  
A:Reference number: Z16207  
A:Accession: T07907  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-446 <R0D>

A:CROSS-references: UNIPROT:O22458; EMBL:AF015883; NID:G2384727; PIDN:AAB69862.1; PID:G  
A:Experimental source: gametes  
C:Genetics:  
A:Gene: GAS28  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-446/Product: hydroxyproline-rich glycoprotein GAS28 #status predicted <MAT>  
Query Match 4.0%; Score 120.5; DB 2; Length 446;  
Best Local Similarity 29.5%; Pred. No. 0.16; Mismatches 46; Gaps 6;  
Matches 38; Conservative 7; Indels 38; Indels 46; Gaps 6;  
QY 320 PGPCCPPPPPPPPSKPTPSLQPA-----GDNPLELSRIPDENCCINRYGHQF 366  
DB 240 PPSPP 299  
QY 367 AT-----TTIVGILEVNI-IQMTDVLMPVPWPRESSLIDFVVTCCGSIPTFVC-----413  
DB 300 MTTASNNTVNVNGLTRICFNVALKDV-----CEN--PNSKCCFELYK 340  
QY 414 TTIISDPTC 421  
DB 341 MEIEADPTC 349

RESULT 8  
C64483  
hypothetical protein MJ1468 - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: C64483  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake  
; Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A  
; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1038-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese,  
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch  
A:Reference number: A64300; MUID:96337999; PMID:8688087  
A:Accession: C64483  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1009 <BUH>  
A:CROSS-references: UNIPROT:Q58863; GB:U67587; GB:L77117; NID:G1592103; PID:G1592109;  
C:Genetics:  
A:Map position: FOR1437031-1440060

Query Match 3.8%; Score 114.5; DB 2; Length 1009;  
Best Local Similarity 18.3%; Pred. No. 1.4;  
Matches 88; Conservative 58; Mismatches 157; Indels 177; Gaps 19;  
QY 100 LIFFRCQKEDANGNIVVEKCRNEAGL-----SADPVYV-----133  
DB 490 LYYPHFVDDNGNI-----EVGIPIPGVGYSSYPQIYASPTIAPTYPIINITIV 541  
QY 134 ---NWT-AMSESDSGNGTQSHNVFPDGKPPHPHGRWRNFIYFHTLGYQFKLGR 189  
DB 542 EPASWTWY-----HHIYFGDGSVWIKPKSPYTFTHYTSEGIV-----582  
QY 190 CSVRVSVNTANVTGLQPMLEVTVRRHGRVPIAQKDVVVVTDQIPVFTMQKNDN 249  
DB 583 -PIYMKVYTAE-----NMKTIVYIDNKNPIAKLYINPAS 617  
QY 250 SSDE-----TFLKDLPI-----FDVLIHDPGSHFLN 275  
DB 618 YKDTISFSPINSYDDANRMIPEVNYGTLGIYPIPSNPMARIYGFNLTVYD-----671  
QY 276 YSTINYKWSFGDNTGLFVSNHTV-NHT-----YVLNGTFLSLNLTVAAPGCPGPP-----326  
DB 672 -SNGVAVNYSSNELTIISKSPFIGNYTAFLVVDGNGVSNVTFVSVINRRPEVAFIY 730  
QY 327 -PPPPPSKP-----TSLGPAGNPLELSRIPDEN-----QINRYGHQFATITI 371  
DB 731 YPKPEPNEDVEFVSQSDPEGLIAYIWNFGDGTINTTDTIVHHKYERPGYVTVLTV 790



```

Query Match      3.6%; Score 109.5; DB 2; Length 348;
Best Local Similarity 21.2%; Pred. No. 0.8;
Matches 83; Conservative 51; Mismatches 128; Indels 129; Gaps 22;

QY      61 VWKRGDMRWKNSWKG--GRVOAVLTSDSPALVGSNITFAVNLIIFRCQKEDANGNIYVEK 118
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      16 VFETGQTKLSATVGNDSATAIIRN--AAGGGIVTVTCVL-----DADGKV--SD 63

QY      119 NCR-NEAGLSADPPVYVNWNTAMSEDSGNGTGCQSHHNVPDPKPPPHHFGWRWNIIYVF 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      64 QCDVHFAAVSAD--IISFSVASDPLGYSNNKA-ARVFAEIIPSNNP---VTNCLINF 117

QY      178 HTLG-----QYFQKLRGCSRVSVNTANVTILGPOLMEVTVYRRHGRAVPIAQVKDVYV 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      118 STFGVGGIINNVYNIIGEPN-----SVSGSPSLMQ-----FVIGNTKTT-- 157

QY      232 VTDOIPEVFTWFOKNDRNSDETFCLKDLPIMFDVLHDPHSFLNYSNTINYKMSFGNTGL 291
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      158 ---IPV-----DVSYKGPE-----EGSVGQAAAL 178

QY      292 FVSTNHTVNHVYLVNGTSL---NLTVKAAAPCCPPPPPPPPPPPSKPTSLGAGDNPLE 348
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      179 VTTTQP-----DKAFALSTPNARVDFINAP-PPPPPPPPSPCCPPPPPPPPPPVR 229

QY      349 LS-----RIPDENCOINRGYFQAATITIVEGILEVNIIOQMTDVLMPVPPESS 396
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      230 PSYTIQIDAVVDNIPIPTCRGDIARVTVFQNGRPLAGALVQCSLVLSG-----NTS 281

QY      397 LIDFVVTCGSGTPEVCTIIISDPTCEITQNT 427
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      282 LM-FALAA-----NEIANLVSP-----QNT 301

```

RESULT 12  
Tl7414  
TipC protein - slime mold (Dictyostelium discoideum)  
C:Species: Dictyostelium discoideum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: Tl7414  
R:Stage, J. T.; Laub, M. T.; Loomis, W. F.  
submitted to the EMBL Data Library, July 1998  
A:Description: Interaction of tip genes in early Dictyostelium discoideum development.  
A:Reference number: Zl8774  
A:Accession: Tl7414  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3848 <STE>  
A:Cross-references: UNIPROT:O76737; EMBL:AF079445; NID:G3420744; PID:G3420745; PIDN:AA  
A:Experimental source: strain AX4  
C:Genetics:  
A:Gene: tipC  
A:Introns: 72/3  
C:Function:  
A:Description: required for tip formation

Query Match	3.6%	Score 108;	DB 2;	Length 3948;
Best Local Similarity	19.0%;	Pred. No. 28;		
Matches	69;	Conservative	55;	Mismatches 132;
				Indels 108;
				Gaps 14;
Qy	3	CLYYFGFLLLAARLPDIAAKRPHDVLGNRPSPAYMREHNLQNLGSSDENDWNEKLYPVM	62	
Db	918	CQVVLVNIQSVTPIDQQQ---	LIGSE--SMYGAFDYSSVYQSNIFKQPQQLPQQ	972
Qy	63	KRGDMRWKNSWKGRRVQAVLTSDSPALVGSNIITFVNLIFFRCOKEDANGNIVYEKNCRN	122	
Db	973	KQ-----	QSPPLISSP-----PLIKKKYSKEFIDSYKMF	1003
Qy	123	EAGLSADPY-----VYNWTAMSEDSGNGTQGSH-----	HNVPDGKFPFHPHGWR	170
Db	1004	EASFNIDKFNIHLRLNDYSGSSNNDSNTTTNNHNLVSHNV-----		1048
Qy	171	WNFIYVFHTLQYFQKLGRCSRVSVN---	TANVTLPQLMEVTYVRHGRAYVPYQVK	227

Db	1049	-ALVYRLCLHGTYYVKQLFDTNLELLIKGMWIEDCFQKPSGI-----AHGSG-----	1099
QY	228	DVYVVTQIPIFVFTMFQKDRN-----SSDETFLKDLPIMFDFVLIHDP	270
Db	1094	-----GDYLATTNRRFKPNDVNIIGGGSNENLIKFKIQIISDSDSPFYNNIDKLDDIELSQI	1148
QY	271	SHFLNYSTINYSKSGFDN-TGLFVSTNHTVNYHYVLNGTFLSLNLTVKAAAPG---PCPPP	326
Db	1149	NLIILNRXTVAGLTIEFSVSNSLSILKKNQNNQ---NNNNNNNNINNESSFTVFTSPPP	1205
QY	327	PPPP 330	
Db	1206	PPPP 1209	

RESULT 13

T23694

hypochemical protein M03C11.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

R:Accession: T23694

R:McMurray, A.

submitted to the EMBL Data Library, April 1995

A:Reference number: Z19783

A:Accession: T23694

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-848 <WIL>

A:Cross-references: UNIPROT:Q21489; EMBL:Z49128; PIDN:CAA88959.1; GSFPDB:GN000211

A:Experimental source: clone M03C11

C:Genetics:

A:Gene: CESP:M03C11.2

A:Map position: 3

A:Introns: 113/2; 147/3; 185/3; 379/1; 482/3; 553/2; 688/3; 762/3

	Query Match	3.5%;	Score 106.5;	DB 2;	Length 848;
	Best Local Similarity	20.8%;	Pred. No. 4.6;		
	Matches 117;	Conservative 75;	Mismatches 203;	Indels 167;	Gaps 30;
QY	83	TSDSPALV--GSNITFAVN-----	LIFPRCQKEDANGNIYVKNCRNEAGLSADP	130	
Db	206	TRFQPRIVTCASRGTLVCNVEVKKLKLNHLINELKCMELKNGMSEKVKQLEKGTTKKT	265		
QY	131	YV-----YNWTAWSDSDG-----	ENGTQGSHHNVPPDGKPF-----	162	
Db	266	KTCATSCFYNSTQIEDVVGVLNSKLSLTLEVSQKGLSNGCYPFATRKSVPOCOLVLL	325		
QY	163	PH-----HPCWRR-W-----	NPFIY-----VPHTLGOYF-----	195	CSV-RVS
Db	326	PYQVLLHDTRKAWGIELKDNVILUDEAHNVUNLTISFFPKLEKVKNGKFNCSLSYAS	385		
QY	196	VNTANVTLLGPQLMEVTVYRRHGRAYV--	PIAQVKDVYVVTDOQIPVFTVMFOKDRNDS	252	
Db	386	ISTKSLLTALRL--IREYNAHYKLLAHLNLYMKQLESLSKMLIFLNSQKSDVMTMA	443		
QY	253	EYFLKDLPMFDVLHDPHFNLNYSTINYKWSFGDNTGLFVSTN----	HTVNHTYVVLNCT	308	
Db	444	Q-LARNLNL-BINLFKALEYMEKTDLCCKFH-----	GEYMRLOKEEIKKENEKPKLTGI	496	
QY	309	FSNLNTVKAAPGCPPPPPPPPPSPKPTP-----	SLGPAGDNPLELSRIPDNCQINRYG	363	
Db	497	QKL-MAAKAEPEPEAEPLPPPKP-VPSPLFSLKSFIDALTNKCEDGRIIVEKSATEAKF	554		
QY	364	HF-----QATITIVGILEVNIIOMTDVMVPVPPESSLIIDFVTVCCGS	407		
Db	555	RFMLLNPADRLSEVWTSARATI-LVGGTME-----	PAQLLVE--TLSRGS	596	
QY	408	IPEVCTIISDPCEITQNTQVSPVDVDSMCLLTVRRRTENGSGTYCVNLTLDGDDTSALTT	467		
Db	597	IGAD-----SIRRFSCCHVIDDSQLAVTVERTVDGPFQLTQYTRGADITLRSLL	646		
QY	468	STLISVPDRDPASPFLRMANSALIS--VGCLAIFFVTVISLL--	YYKHKHKNPIENSPGNNV	523	



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 19, 2004, 14:50:36 ; Search time 39 Seconds  
(without alignments)  
952.258 Million cell updates/sec

Title: US-09-853-880A-17

Perfect score: 3026

Sequence: 1 MECLYVFLGLLLAARPLD.....FPCNQEKDPLLKNQEFKGVY 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/6C\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3026	100.0	560	1	US-09-985-799-90
2	3026	100.0	560	1	US-09-977-371-90
3	3026	100.0	560	1	US-08-594-031-90
4	3026	100.0	560	4	US-09-643-597-225
5	3026	100.0	560	4	US-09-480-884A-225
6	3026	100.0	560	4	US-09-542-615A-225
7	3026	100.0	560	4	US-09-606-421B-225
8	3026	100.0	560	4	US-09-476-496A-225
9	3026	100.0	560	4	US-09-630-940B-225
10	2197	72.6	574	3	US-09-383-586-36
11	2197	72.6	574	4	US-09-823-038A-36
12	2179	72.0	572	4	US-09-197-970B-5
13	969	32.0	376	1	US-09-985-799-100
14	969	32.0	376	1	US-09-985-799-102
15	969	32.0	376	1	US-09-977-371-100
16	969	32.0	376	1	US-09-977-371-102
17	969	32.0	376	1	US-08-594-031-100
18	969	32.0	376	1	US-08-594-031-102
19	622	20.6	661	2	US-08-417-174-121
20	622	20.6	661	3	US-09-267-439-121
21	622	20.6	661	4	US-08-388-852B-2
22	622	20.6	661	4	US-09-073-138-121
23	621	20.5	661	2	US-08-417-174-27
24	621	20.5	661	2	US-08-231-565A-27
25	621	20.5	661	2	US-09-007-961-27
26	621	20.5	661	3	US-09-267-439-27
27	621	20.5	661	4	US-09-073-138-27

28 603.5 19.9 668 1 US-07-891-942G-6 Sequence 6, Appl  
29 238.5 7.9 190 4 US-08-388-852B-35 Sequence 35, Appl  
30 236 7.8 202 4 US-08-388-852B-38 Sequence 38, Appl  
31 233.5 7.7 192 4 US-08-388-852B-37 Sequence 37, Appl  
32 233 7.7 197 4 US-08-388-852B-36 Sequence 36, Appl  
33 136.5 4.5 71 1 US-09-985-799-98 Sequence 98, Appl  
34 136.5 4.5 71 1 US-09-977-371-98 Sequence 97, Appl  
35 136.5 4.5 71 1 US-08-594-031-98 Sequence 98, Appl  
36 116 3.8 742 4 US-09-489-039A-7998 Sequence 98, Appl  
37 112 3.7 440 4 US-09-248-796A-26860 Sequence 26860, A  
38 111 3.7 429 4 US-09-252-991A-31611 Sequence 31611, A  
39 108 3.6 1158 4 US-09-313-942-26 Sequence 26, Appl  
40 108 3.6 4302 3 US-08-658-136-5 Sequence 5, Appl  
41 107.5 3.6 4302 3 US-08-658-136-5 Sequence 5, Appl  
42 106 3.5 859 4 US-09-313-942-7 Sequence 7, Appl  
43 105.5 3.5 427 3 US-08-705-771-16 Sequence 16, Appl  
44 105.5 3.5 427 4 US-09-417-540-16 Sequence 16, Appl  
45 105.5 3.5 4303 2 US-08-460-751-2 Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-985-799-90  
; Sequence 90, Application US/09985799  
; Patent No. RE38392  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Timothy C.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/985,799  
; FILING DATE: 06-NOV-1995  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,031  
; FILING DATE: 30-JAN-1996  
; APPLICATION NUMBER: 60/006,838  
; FILING DATE: 16-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Remenick, James  
; REGISTRATION NUMBER: 36,902  
; REFERENCE/DOCKET NUMBER: 0A146-0110  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-639-7700  
; TELEFAX: 202-639-7890  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 90:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 560 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:

US-09-985-799-90

Query Match 100.0%; Score 3026; DB 1; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.9e-269;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
DB 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
QY 61 VMKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVVEKNC 120  
DB 61 VMKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVVEKNC 120  
QY 121 RNEAGLSADPYVYVNTAWSEDSGNGTGSHNVFPDGPFPHPGWRWNFIYVFHTL 180  
DB 121 RNEAGLSADPYVYVNTAWSEDSGNGTGSHNVFPDGPFPHPGWRWNFIYVFHTL 180  
QY 181 GQYFQKLGRCVRSVNTANVTLGPMQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
DB 181 GQYFQKLGRCVRSVNTANVTLGPMQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
QY 241 TMFQKNDNRSSDFTFLKDLPIPMFDVLIHDPESHFNLYSTINYSKWSFGDNTGLFVSTNHTVN 300  
DB 241 TMFQKNDNRSSDFTFLKDLPIPMFDVLIHDPESHFNLYSTINYSKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTVVLNGTFSNLNLTVKAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIIPDENCQIN 360  
DB 301 HTVVLNGTFSNLNLTVKAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIIPDENCQIN 360  
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVVTCCGSIPTVECTIISDPT 420  
DB 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVVTCCGSIPTVECTIISDPT 420  
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGLDGTSLALTSTLISVPDRDPAS 480  
DB 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGLDGTSLALTSTLISVPDRDPAS 480  
QY 481 PLRMANSALISVGCLAIFFTVISLLVYKHKHKEYNPINSPGNVVRSGLSVFLNRAKAVF 540  
DB 481 PLRMANSALISVGCLAIFFTVISLLVYKHKHKEYNPINSPGNVVRSGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLNKQEFKGVNS 560  
DB 541 FPGNQEKDPLLNKQEFKGVNS 560

RESULT 2  
US-09-977-371-90  
; Sequence 90, Application US/09977371  
; Patent No. RE38490  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Timothy C.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/977,371  
; FILING DATE: 16-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,031  
; FILING DATE: 30-JAN-1996

APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 560 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 90:  
US-09-977-371-90

Query Match 100.0%; Score 3026; DB 1; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.9e-269;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
DB 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
QY 61 VMKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVVEKNC 120  
DB 61 VMKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIIPRCKEDANGNIVVEKNC 120  
QY 121 RNEAGLSADPYVYVNTAWSEDSGNGTGSHNVFPDGPFPHPGWRWNFIYVFHTL 180  
DB 121 RNEAGLSADPYVYVNTAWSEDSGNGTGSHNVFPDGPFPHPGWRWNFIYVFHTL 180  
QY 181 GQYFQKLGRCVRSVNTANVTLGPMQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
DB 181 GQYFQKLGRCVRSVNTANVTLGPMQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
QY 241 TMFQKNDNRSSDFTFLKDLPIPMFDVLIHDPESHFNLYSTINYSKWSFGDNTGLFVSTNHTVN 300  
DB 241 TMFQKNDNRSSDFTFLKDLPIPMFDVLIHDPESHFNLYSTINYSKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTVVLNGTFSNLNLTVKAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIIPDENCQIN 360  
DB 301 HTVVLNGTFSNLNLTVKAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIIPDENCQIN 360  
QY 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVVTCCGSIPTVECTIISDPT 420  
DB 361 RYGHFOATITIVEGILEVNIQMTDVLMPVPWPESSLIIDFVVTCCGSIPTVECTIISDPT 420  
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGLDGTSLALTSTLISVPDRDPAS 480  
DB 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTGLDGTSLALTSTLISVPDRDPAS 480  
QY 481 PLRMANSALISVGCLAIFFTVISLLVYKHKHKEYNPINSPGNVVRSGLSVFLNRAKAVF 540  
DB 481 PLRMANSALISVGCLAIFFTVISLLVYKHKHKEYNPINSPGNVVRSGLSVFLNRAKAVF 540  
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DB 541 FPGNQEKDPLLNKQEFKGVNS 560

RESULT 3  
US-08-594-031-90  
; Sequence 90, Application US/08594031  
; Patent No. 5783182



Db	361	RYGHFQATITIV	EGLEVNIIQMTDVLMPVPPESSLDIFVVTQCSIPTEVCIIISDPT	420
Qy	421	CBITQNTVCS	PVDVDEMCLLTVRRITFNGSGTYCVNLTLGGDDTSLALTSLTSLISVPDRDPAS	480
Db	421	CBITQNTVCS	PVDVDEMCLLTVRRITFNGSGTYCVNLTLGGDDTSLALTSLTSLISVPDRDPAS	480
Qy	481	PLRMANSALIS	VGCLAIFFVTVISLIVYKKGHKYNPNIENSPGNVRSKGLSVFLNRAKAVF	540
Db	481	PLRMANSALIS	VGCLAIFFVTVISLIVYKKGHKYNPNIENSPGNVRSKGLSVFLNRAKAVF	540
Qy	541	FPGNOEKDPL	LKNQBFKGS	560
Db	541	FPGNOEKDPL	LKNQBFKGS	560
<div> <div>RESULT 4</div> <div> US-09-643-597-225  ; Sequence 225, Application US/09643597  ; Patent No. 6426072  ; GENERAL INFORMATION:  ; APPLICANT: Wang, Tongtong  ; APPLICANT: Fan, Liqun  ; APPLICANT: Kalos, Michael D.  ; APPLICANT: Bangur, Chaitanya S.  ; APPLICANT: Hosken, Nancy  ; APPLICANT: Fanger, Gary R.  ; APPLICANT: Li, Samuel X.  ; APPLICANT: Wang, Aijun  ; APPLICANT: Skeiky, Yasir A.W.  ; APPLICANT: Henderson, Robert A.  ; APPLICANT: McNeill, Patricia D.  ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  ; FILE REFERENCE: 210121.455C11  ; CURRENT APPLICATION NUMBER: US/09/643,597  ; CURRENT FILING DATE: 2000-08-21  ; NUMBER OF SEQ ID NOS: 369  ; SOFTWARE: FASTSEQ for Windows Version 3.0  ; SEQ ID NO 225  ; LENGTH: 560  ; TYPE: PRT  ; ORGANISM: Homo sapien  US-09-643-597-225 </div> </div>				
Query Match 100.0%; Score 3026; DB 4; Length 560; Best Local Similarity 100.0%; Pred. No. 4.9e-269; Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	MECLYYFLG	ELLAAARLPDAAKRFHDVLGNRPSAYMREHNLQNGSSDENDWNEKLYP	60
Db	1	MECLYYFLG	ELLAAARLPDAAKRFHDVLGNRPSAYMREHNLQNGSSDENDWNEKLYP	60
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Db	61	VWKGDMRWKN	SKWGRVQAVLTSDSPALVGSNITFAVNLIIFRCOKEDANGNIYVEKNC	120
Qy	121	RNEAGLSADP	PYYVNTAWSDSDSGENTGQSHNVFPDGKFPFPHPCWRWNFYIVVHTL	180
Db	121	RNEAGLSADP	PYYVNTAWSDSDSGENTGQSHNVFPDGKFPFPHPCWRWNFYIVVHTL	180
Qy	181	GQYFQKLG	RCSVRVSVNTANVTLGPMOLMEVTVYRRHGRAYPIAQVKDVVVVTDQIPFVF	240
Db	181	GQYFQKLG	RCSVRVSVNTANVTLGPMOLMEVTVYRRHGRAYPIAQVKDVVVVTDQIPFVF	240
Qy	241	TFWQKDRNS	SDETELKDIPIMFEDVLHDPHSFNLSTINYKWSFGDNTGLFVSTNHTVN	300
Db	241	TFWQKDRNS	SDETELKDIPIMFEDVLHDPHSFNLSTINYKWSFGDNTGLFVSTNHTVN	300
Qy	301	HTYVLNGT	FSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIPENDNCQIN	360
Db	301	HTYVLNGT	FSNLTVKAAAPGCPPPPPRPSKPTPSLGPAGDNPLELSRIPENDNCQIN	360

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QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
QY 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPNIENSPGNVVRSGLSVFLNRAKAVF 540
Db 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPNIENSPGNVVRSGLSVFLNRAKAVF 540
QY 541 PFGNOEKDPLLKNQBFKGV 560
Db 541 PFGNOEKDPLLKNQBFKGV 560
QY 541 PFGNOEKDPLLKNQBFKGV 560
Db 541 PFGNOEKDPLLKNQBFKGV 560

RESULT 6
US-09-542-615A-225
; Sequence 225, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-542-615A-225

Query Match 100.0%; Score 3026; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-269;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFFRCOKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFFRCOKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTOGSHNVFPDGPFPHPGWRWNFIYVFHTL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTOGSHNVFPDGPFPHPGWRWNFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANTVLTGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPFV 240
Db 181 GOYFQKLGRCVRSVNTANTVLTGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPFV 240
QY 241 TMEQKNDNRSSDDETFKDLPIFMDVLIHDSHFLNYSNTINXKWSFGDNTGLFVSTNHTN 300
Db 241 TMEQKNDNRSSDDETFKDLPIFMDVLIHDSHFLNYSNTINXKWSFGDNTGLFVSTNHTN 300
QY 301 HTYVLNGTFSNLNITVKAAPGCPPPPPRPSKPTSLGPDAGNPLELSRIPDENCQIN 360
Db 301 HTYVLNGTFSNLNITVKAAPGCPPPPPRPSKPTSLGPDAGNPLELSRIPDENCQIN 360
QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
QY 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPNIENSPGNVVRSGLSVFLNRAKAVF 540
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QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
Db 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
QY 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPNIENSPGNVVRSGLSVFLNRAKAVF 540
Db 481 PLRMANALISVGCCLAIFVTVISLLVYKHKKEYNPNIENSPGNVVRSGLSVFLNRAKAVF 540
QY 541 PFGNOEKDPLLKNQBFKGV 560
Db 541 PFGNOEKDPLLKNQBFKGV 560

RESULT 5
US-09-480-884A-225
; Sequence 225, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-480-884A-225

Query Match 100.0%; Score 3026; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 4.9e-269;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGSSDENDWNEKLYP 60
Db 1 MECLYYFLGFLLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGSSDENDWNEKLYP 60
QY 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFFRCOKEDANGNIVYEKNC 120
Db 61 VKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITPAVNLIFFRCOKEDANGNIVYEKNC 120
QY 121 RNEAGLSADPYVYNWTAWSESDSGENGTOGSHNVFPDGPFPHPGWRWNFIYVFHTL 180
Db 121 RNEAGLSADPYVYNWTAWSESDSGENGTOGSHNVFPDGPFPHPGWRWNFIYVFHTL 180
QY 181 GOYFQKLGRCVRSVNTANTVLTGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPFV 240
Db 181 GOYFQKLGRCVRSVNTANTVLTGPQLMEVTVYRRHGRAYVPTAQVKDVVVTDDQIPFV 240
QY 241 TMEQKNDNRSSDDETFKDLPIFMDVLIHDSHFLNYSNTINXKWSFGDNTGLFVSTNHTN 300
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Db 301 HTYVLNGTFSNLNITVKAAPGCPPPPPRPSKPTSLGPDAGNPLELSRIPDENCQIN 360
QY 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
Db 361 RYGHFQATITIVGILEVNIITQMTDVLMPVWPWESSLIDFVVTCCGSIPTVEVCTIISDPT 420
QY 421 CEITQNTVCSVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLATSTLISVDPDRPAS 480
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Db 481 PLRMANALISVGCCLAFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLKNQEFKGV 560  
Db 541 FPGNQEKDPLLKNQEFKGV 560

## RESULT 7

US-09-606-421B-225  
; Sequence 225, Application US/09606421B  
; Patent No. 6531315  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liyun  
; APPLICANT: Kaloe, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606,421B  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-606-421B-225

Query Match 100.0%; Score 3026; DB 4; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.9e-269;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60  
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QY 181 GOYFQKLGRCVRSVSVNTANTLGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240  
Db 181 GOYFQKLGRCVRSVSVNTANTLGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240  
QY 241 TMFQKNDNSDETFLKDLPIMFVDLIHDPSSHFLNYSTINYSKSGDNTGLFVSTNHTVN 300  
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QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLELSRIPDENCQIN 360  
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLELSRIPDENCQIN 360  
QY 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPRESSLIDFVTCQGSIPTEVCTIISDPT 420  
Db 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPRESSLIDFVTCQGSIPTEVCTIISDPT 420  
QY 421 CEITQNTVCSVPVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLALTSLISVDRDPAS 480  
Db 421 CEITQNTVCSVPVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLALTSLISVDRDPAS 480  
QY 481 PLRMANALISVGCCLAFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PLRMANALISVGCCLAFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540

Db 481 PLRMANALISVGCCLAFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLKNQEFKGV 560  
Db 541 FPGNQEKDPLLKNQEFKGV 560

## RESULT 8

US-09-476-496A-225  
; Sequence 225, Application US/09476496A  
; Patent No. 6706262  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF  
; FILE REFERENCE: 210121.455C5  
; CURRENT APPLICATION NUMBER: US/09/476,496A  
; NUMBER OF SEQ ID NOS: 254  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-476-496A-225

Query Match 100.0%; Score 3026; DB 4; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4.9e-269;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60  
Db 1 MECLYFGLFLLAARLPDAAKRFHDVLGNRPSPAYMRHNLQNGWSSDENDWNEKLYP 60  
QY 61 VMKGRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPPRCQKEDANGNIYVEKNC 120  
Db 61 VMKGRDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPPRCQKEDANGNIYVEKNC 120  
QY 121 RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVFPDGKPPHHPGRRWNFIYVPHL 180  
Db 121 RNEAGLSADPYVYNWNTAWSESDSGENGTCQSHHNVFPDGKPPHHPGRRWNFIYVPHL 180  
QY 181 GOYFQKLGRCVRSVSVNTANTLGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240  
Db 181 GOYFQKLGRCVRSVSVNTANTLGPQMEVTVYRRHGRAYVPIAQVKDVVVTDQIPVFV 240  
QY 241 TMFQKNDNSDETFLKDLPIMFVDLIHDPSSHFLNYSTINYSKSGDNTGLFVSTNHTVN 300  
Db 241 TMFQKNDNSDETFLKDLPIMFVDLIHDPSSHFLNYSTINYSKSGDNTGLFVSTNHTVN 300  
QY 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLELSRIPDENCQIN 360  
Db 301 HTYVLNGTFSNLTVKAAAPGCPPPPSPKPTPSLGPAGDNPLELSRIPDENCQIN 360  
QY 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPRESSLIDFVTCQGSIPTEVCTIISDPT 420  
Db 361 RYGHFQATITIVGILEVNIQMTDVLMPVPWPRESSLIDFVTCQGSIPTEVCTIISDPT 420  
QY 421 CEITQNTVCSVPVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLALTSLISVDRDPAS 480  
Db 421 CEITQNTVCSVPVDVDEMCLLTVRRTFNGSGTYCVNLTGLDDTSLALTSLISVDRDPAS 480  
QY 481 PLRMANALISVGCCLAFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540  
Db 481 PLRMANALISVGCCLAFVTVISLLVYKKHKEYNPISNPGNVRSKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLKNQEFKGV 560  
Db 541 FPGNQEKDPLLKNQEFKGV 560

RESULT 9  
US-09-630-940B-225  
; Sequence 225, Application US/09630940B  
; Patent No. 6737514  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C10  
; CURRENT APPLICATION NUMBER: US/09/630,940B  
; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 367  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 225  
; LENGTH: 560  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-630-940B-225

Query Match 100.0%; Score 3026; DB 4; Length 560;  
Best Local Similarity 100.0%; Pred. No. 4,9e-269; Mismatches 0; Indels 0; Gaps 0;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MECLYYFLGFLLLAARPLDAAKRFHVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
DB 1 MECLYYFLGFLLLAARPLDAAKRFHVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
QY 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIVVEKNC 120  
DB 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIVVEKNC 120  
QY 121 RNEAGLSADPYVYNWNTAWSDSDGNGTGHSHNVFPDGPFPHPGWRWNFIYVPHTL 180  
DB 121 RNEAGLSADPYVYNWNTAWSDSDGNGTGHSHNVFPDGPFPHPGWRWNFIYVPHTL 180  
QY 181 GOYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
DB 181 GOYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
QY 241 TMFQKDRNSDDETFKDLPIMEDVLIHDSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
DB 241 TMFQKDRNSDDETFKDLPIMEDVLIHDSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
QY 301 HTVVLNGTFSNLTVKAAAPGCPFPFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 360  
DB 301 HTVVLNGTFSNLTVKAAAPGCPFPFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 360  
QY 361 RYGHFOATITIVGILEVNIQMTDVLMPWPWESSLIDFVVTCCGSIPTVECTIISDPT 420  
DB 361 RYGHFOATITIVGILEVNIQMTDVLMPWPWESSLIDFVVTCCGSIPTVECTIISDPT 420  
QY 421 CEITQNTVCSVDVDEMCLLTVRETENGSGTYCVNLTGDDTSLALSTLISVDPDRPAS 480  
DB 421 CEITQNTVCSVDVDEMCLLTVRETENGSGTYCVNLTGDDTSLALSTLISVDPDRPAS 480  
QY 481 PLRMANGALISVGCLAFVTVISLLVYKKHKEYNPIENSPGNVVRKGLSVFLNRAKAVF 540  
DB 481 PLRMANGALISVGCLAFVTVISLLVYKKHKEYNPIENSPGNVVRKGLSVFLNRAKAVF 540  
QY 541 FPGNQEKDPLLNQEFKGV 560  
DB 541 FPGNQEKDPLLNQEFKGV 560

Query Match 72.6%; Score 2197; DB 3; Length 574;  
Best Local Similarity 70.7%; Pred. No. 6.3e-193; Mismatches 69; Indels 16; Gaps 2;  
Matches 403; Conservative 69; Mismatches 82; Indels 16; Gaps 2;  
QY 1 MECLYYFLGFLLLAARPLDAAKRFHVLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60  
DB 1 MESLGVGLGLLLAAGLPQAAKRFHVLGHEQYPNHREHNLQNGSSDENEWDHLYP 60  
QY 61 VKRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIVVEKNC 120  
DB 61 VMRRGDMRWKNSKGRVQAVLTSDSPALVGSNITFAVNLIFFRCQKEDANGNIVVEKNC 120  
QY 121 RNEAGLSADPYVYNWNTAWSDSDGNGTGHSHNVFPDGPFPHPGWRWNFIYVPHTL 180  
DB 121 RNDLGUTSDUHVYNWNTAGADDGWDGTSRSHLRFPDRPFPFPHGKWSFVYVPHTL 180  
QY 181 GOYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
DB 181 GOYFQKLGRCVRSVNTANVTGLPQMEVTVYRRHGRAYVPIAQVKDVVVTDDQIPVFV 240  
QY 241 TMFQKDRNSDDETFKDLPIMEDVLIHDSHFLNYSNTYKWSFGDNTGLFVSTNHTVN 300  
DB 241 TMSQKDRNLSDIEFLRDLPIFVDFLIHDSHFLNYSNTYKWSFGDNTGLFVSTNHTLN 300  
QY 301 HTVVLNGTFSNLTVKAAAPGCPFPFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 344  
DB 301 HTVVLNGTFSNLTVKAAAPGCPFPFPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 360  
QY 345 NPLESRIIPDENCOINRYGHFOATITIVGILEVNIQMTDVLMPWPWESSLIDFVVTCC 404  
DB 361 KSMELSDISNENCRINRYGYFRATITIVGILEVSIQIADVPMTQPANSLMDFVTVC 420  
QY 405 QGSIPTVECTIISDPTCEITQNTVCSVDVDEMCLLTVRETENGSGTYCVNLTGDDTSL 464  
DB 421 KGATPEACTIISDPTCEITQNTVCSVDVDEMCLLTVRETENGSGTYCVNLTGDDTSL 480  
QY 465 ALATSTLISVDPDRPASPLRMANGALISVGCLAFVTVISLLVYKKHKEYNPIENSPGNV 524  
DB 481 ALATSTLISVDPDRPASPLRMANGALISVGCLAFVTVISLLVYKKHKEYNPIENSPGNV 540  
QY 525 RSKGLSVFLNRAKAVFPFPGNQEKDPLLNQ 554  
DB 541 KGKGLSVLLSHAKAPFPGNQEKDPLLNQ 570

RESULT 11  
US-09-823-038A-36

Sequence 36, Application US/09823038A

Patent No. 6797271

GENERAL INFORMATION:

APPLICANT: Strachan, Lorna

APPLICANT: Sleeman, Matthew

APPLICANT: Abernethy, Nevin

APPLICANT: Onrust, Rene

APPLICANT: Kumble, Anand

APPLICANT: Murison, Greg

TITLE OF INVENTION: Compositions Isolated From Stromal Cells

TITLE OF INVENTION: and Methods For Their Use

FILE REFERENCE: 11000.1037c3

CURRENT APPLICATION NUMBER: US/09/823,038A

CURRENT FILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 61

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 36

LENGTH: 574

TYPE: PRT

ORGANISM: Mouse

US-09-823-038A-36

Query Match

Best Local Similarity 72.8%; Score 2197; DB 4; Length 574;

Mismatches 70.7%; Pred. No. 6.3e-193;

Matches 403; Conservative 69; Mismatches 82; Indels 16; Gaps 2;

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QY 1 MECLYVFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
DB 1 MESLGVFLGFLLLAAGLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIYVEKNC 120
DB 61 VWRGDRGWKDSWEGGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVNTWTAWSESDGNGTQSHHNVFPDGPFPHPGRRWFIYVFTL 180
DB 121 RNDGLTSLDHYNTWTAGADGWDGTSRQHLRFDPDRPFRPHGKWKSWFIYVFTL 180
QY 181 GOYFQKLGRCVSRSVNTANVTGLGOLMEVTVYRRHGRAYPIAQVKDYVVTDOIPVFV 240
DB 181 GOYFQKLGRCVSRSVNTANVTGLGOLMEVTVYRRHGRAYPIAQVKDYVVTDOIPVFV 240
QY 241 TMFQKDRNSDETFLKDLPIFMDVLIHDPVSHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMSQKDRNSDETFLRDLPIFMDVLIHDPVSHFLNYSTINYKWSFGDNTGLFVSTNHTLN 300
QY 301 HTYVLNGTFSNLTVKAAPGCP-----PPPPPPR-----SKTPSLGPAGD 344
DB 301 HTYVLNGTFSNLTVKAAPGCP-----PPPPPPR-----SKTPSLGPAGD 344
QY 345 NPLESRIPEQNCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIFVVTVC 404
DB 345 NPLESRIPEQNCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIFVVTVC 404
QY 405 QGSIPTEVCTIISDPTCEITQNTGSPVDVDEMCLLTVRRTPNGSGTVCNLTLLGDDTSL 464
DB 405 QGSIPTEVCTIISDPTCEITQNTGSPVDVDEMCLLTVRRTPNGSGTVCNLTLLGDDTSL 464
QY 421 KGATMEACTIISDPTCQIAQNRVCSVAVDGLCLLSVRRFNGSGTVCNLTLLGDDTSL 480
DB 421 KGATMEACTIISDPTCQIAQNRVCSVAVDGLCLLSVRRFNGSGTVCNLTLLGDDTSL 480
QY 465 ALTSTLISVPRDPAASPRMANSALISVGCIAFVTVISLIVYKHKKEYNFIENSPGNV 524
DB 465 ALTSTLISVPRDPAASPRMANSALISVGCIAFVTVISLIVYKHKKEYNFIENSPGNV 524
QY 481 ALTSTLISIPKDPSPRAVNGVLISIGCLAVLTMTVITLLYKHKKAYKPIGNCPRTV 540
DB 481 ALTSTLISIPKDPSPRAVNGVLISIGCLAVLTMTVITLLYKHKKAYKPIGNCPRTV 540
QY 525 RSKGLSVFLNRAKAVFFPGNOEKDPLLNQ 554
DB 525 RSKGLSVFLNRAKAVFFPGNOEKDPLLNQ 554
QY 541 KGKGLSVLLSHAKAPFFRGDQEKDPLLNQ 570
DB 541 KGKGLSVLLSHAKAPFFRGDQEKDPLLNQ 570
```

RESULT 12

US-09-197-970B-5

Sequence 5, Application US/09197970B

Patent No. 6664385

GENERAL INFORMATION:

APPLICANT: Michele Sanicola-Nadel

Joseph V. Bonventre  
Catherine A. Hession  
Takaharu Ichimura  
Henry Wei  
Richard L. Cate

TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center

CITY: Cambridge

STATE: MA

COUNTRY: USA

ZIP: 02142

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/197,970B

FILING DATE: 23-No. 6664385-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/018,228

FILING DATE: 24-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Levine, Leslie M.

REGISTRATION NUMBER: 35,245

REFERENCE/DOCKET NUMBER: A010 PCT CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 679-2810

TELEFAX: (617) 679-2838

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 572 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-197-970B-5

Query Match

Best Local Similarity 72.0%; Score 2179; DB 4; Length 572;

Mismatches 69.7%; Pred. No. 2.8e-191;

Matches 396; Conservative 74; Mismatches 84; Indels 14; Gaps 1;

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QY 1 MECLYVFLGFLLLAARLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
DB 1 MESLGVFLGFLLLAAGLPDAAKRFHDLGNRPSPAYMREHNLQNGSSDENDWNEKLYP 60
QY 61 VVKRGDMRWKNSWKGGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIYVEKNC 120
DB 61 VWRGDRGWKDSWEGGRVQAVLTSDSPALVGSNITFAVNLIPRCCKEDANGNIYVEKNC 120
QY 121 RNEAGLSADPYVNTWTAWSESDGNGTQSHHNVFPDGPFPHPGRRWFIYVFTL 180
DB 121 RNDGLTSLDHYNTWTAGADGWDGTSRQHLRFDPDRPFRPHGKWKSWFIYVFTL 180
QY 181 GOYFQKLGRCVSRSVNTANVTGLGOLMEVTVYRRHGRAYPIAQVKDYVVTDOIPVFV 240
DB 181 GOYFQKLGRCVSRSVNTANVTGLGOLMEVTVYRRHGRAYPIAQVKDYVVTDOIPVFV 240
QY 241 TMFQKDRNSDETFLKDLPIFMDVLIHDPVSHFLNYSTINYKWSFGDNTGLFVSTNHTVN 300
DB 241 TMSQKDRNSDETFLRDLPIFMDVLIHDPVSHFLNYSTINYKWSFGDNTGLFVSTNHTLN 300
QY 301 HTYVLNGTFSNLTVKAAPGCP-----PPPPPPR-----SKTPSLGPAGDNP 346
DB 301 HTYVLNGTFSNLTVKAAPGCP-----PPPPPPR-----SKTPSLGPAGDNP 346
QY 347 LEISRIPEQNCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIFVVTVC 406
DB 347 LEISRIPEQNCQINRYGHFOATITIVGILEVNIQMTDVLMPVPWPESSLDIFVVTVC 406
QY 361 MEISDISNENCRINRYGYFRATITIVGILEVNIQVADVPITPQPDNSLMDIFVTCG 420
DB 361 MEISDISNENCRINRYGYFRATITIVGILEVNIQVADVPITPQPDNSLMDIFVTCG 420
```

QY	407	SIPTVECTIISDPTCEITONTVCSPVDVDEMCLLTVRRTFNGSGTYCVNLTIGDDTSLAL	466
Db	421	ATPTEACTIISDPTCQIAQNRVCSPVAVDELCLLSVRRAFNGSGTYCVNFTLGGDASLAL	480
QY	467	TSTLSVDPDRDPASPLRMANSALISVGCIAFTVTVLSLAVYKKHKEYNPIENSGNVRS	526
Db	481	TSALISIPGKLGSPURTNGVLISIGCLAMFTVMTVILLYKKHKEYKPIGNCNTRNVKG	540
QY	527	KGSLVFLNRAKAVFFPGNQEKDPLLNQ	554
Db	541	KGSLVFLSHAKAFFSRGDKREKPLLOQK	568
RESULT 13			
US-09-985-799-100			
; Sequence 100, Application US/09985799			
; Patent No. RE38392			
; GENERAL INFORMATION:			
; APPLICANT: THOMPSON, Timothy C.			
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES			
; NUMBER OF SEQUENCES: 175			
; CORRESPONDENCE ADDRESS:			
; ADDRESSER: BAKER & BOTTS, L.L.P.			
; STREET: 1299 Pennsylvania Avenue, N.W.			
; CITY: Washington			
; STATE: DC			
; COUNTRY: USA			
; ZIP: 20004-2400			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Diskette			
; OPERATING SYSTEM: DOS			
; SOFTWARE: FastSEQ Version 1.5			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/985,799			
; FILING DATE: 06-NOV-1995			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/594,031			
; FILING DATE: 30-JAN-1996			
; APPLICATION NUMBER: 60/006,838			
; FILING DATE: 16-NOV-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Remenick, James			
; REGISTRATION NUMBER: 36,902			
; REFERENCE/DOCKET NUMBER: 0A146-0110			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 202-639-7700			
; TELEFAX: 202-639-7890			
; TELEX: <Unknown>			
; INFORMATION FOR SEQ ID NO: 100:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 376 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: peptide			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; FRAGMENT TYPE: N-terminal			
; ORIGINAL SOURCE:			
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:			
US-09-985-799-100			
Query Match			
Best Local Similarity			
Matches 298; Conservative 26; Mismatches 47; Indels 176; Gaps 60;			
32.0%; Score 969; DB 1; Length 376;			
54.5%; Pred. No. 1.8e-80;			
14 AARPLDAAKPHVILGNRPSAYRHNQNLNGWSSDNDNEKLYPVWKGDWRKNSW			
73			
6 AAR---DAKR-HDV-GNR--SAYMR-HN--NGWSSD-NDWKY---VWKRGDWRKNSW			
51			
Db			

QY	74	KGRRVOAVLTSDPALVGSNITFAVNLIFPRCKEDANGNIYVEKNCRNEAGLSADPPYV	133
Db	52	KGRRV--AVTSDS--AVGSNT--AYN-----RC--KDANGNVY--KNCRN-AG-SAD-YYV	94
QY	134	NWTAMSESDGSENGTGQSHNVFPDGKPPHPHRRRNFIYVHTLGGYFQKLGRCVSR	193
Db	95	NWTAMS--DSDG--NGTG--SHNV--DCK-----HHGWRRNWYVHTGYK-----GRCSVR	137
QY	194	VSVNTANVTGLPQLMEVTVYRHHGRAYVPIAOVKDYYVVTDQIPVFTVMFQKNDRNSSDE	253
Db	138	VSVNTANVT-----GKMTVYRHHGRAYV---AVKDVYVVVD-----VVTM--KNDRNSSDT	183
QY	254	TELKDLPIPMFDVLIHDPGSHFLNYSINYKWSFGDNTGLFVSTNHTVNNHTYVNLNGTSLNL	313
Db	184	K-----DMDVHD-SH--NYST--NYKWS--GDNTG--VSTNHTVNNHTYV--NGTSN---	223
QY	314	TVKAAAGPCPPPPPPRPSKTPSLGPDAGNPLSLRIPDENCQINRNGHQAATITVE	373
Db	224	TVKAAA--GC-----RSKTSAGDN---SR---DNC--NRYGH---ATTVG	256
QY	374	GILEVNIQMTDVLMPVPMPPESSLIDFVVTCCGSIPTVEVCTIISDPTCEITONTVCSPVD	433
Db	257	-----VNMIDVMV---WSSD-----VUTC-GS-----TVCTSDTC--TNTVCS-VD	290
QY	434	VDEMCLLTVRRTPNGSGTYCVNLTGLGDDTSLATSTLISVPDRDPASPLRMANSALISVG	493
Db	291	VD-MC--TVRRT--NGSGTYCVN--TGDDTSATSTSV-----DRDAS--RMANSA--SVG	334
QY	494	CLAIFVTVISLLVYKHKKEYNPIENSGNVRSKGLSVFLNRAKAVFFPGNQEKDPLLN	553
Db	335	C-----AVTVSVYKHK-----YNNSGNVRSKGLSVFLNRAKAV---SVNRAKAV---GNKDKN	372
QY	554	QBEFGVS	560
Db	373	---KGVS	376

RESULT 14

US-09-985-799-102

; Sequence 102, Application US/09985799

; Patent No. RE38392

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BAKER & BOTTS, L.L.P.

; STREET: 1299 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004-2400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/985,799

; FILING DATE: 06-NOV-1995

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/594,031

; FILING DATE: 30-JAN-1996

; APPLICATION NUMBER: 60/006,838

; FILING DATE: 16-NOV-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Remenick, James

; REGISTRATION NUMBER: 36,902

; REFERENCE/DOCKET NUMBER: 0A146-0110

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-639-7700

; TELEFAX: 202-639-7890

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 100:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 376 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-09-985-799-100

Query Match

Best Local Similarity

Matches 298; Conservative 26; Mismatches 47; Indels 176; Gaps 60;

32.0%; Score 969; DB 1; Length 376;

54.5%; Pred. No. 1.8e-80;

14 AARPLDAAKPHVILGNRPSAYRHNQNLNGWSSDNDNEKLYPVWKGDWRKNSW

73

6 AAR---DAKR-HDV-GNR--SAYMR-HN--NGWSSD-NDWKY---VWKRGDWRKNSW

51

Db

TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 102:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 102:  
US-09-985-799-102

Query Match 32.0%; Score 969; DB 1; Length 376;  
Best Local Similarity 54.5%; Pred. No. 1.8e-80;  
Matches 298; Conservative 26; Mismatches 47; Indels 176; Gaps 60;

14 AARPLDAAKRFHDLGNRPSAYMRHNLQNGSSDNDWNEKLYPVWKGDMRWKNSW 73  
6 AAR---DAKR-HDV-GNR--SAYMR-HN--NGWSSD-NDWNY---VWKGDMRWKNSW 51  
74 KGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIYVYKNCNEAGLSADPYVY 133  
52 KGRV--AVTSDS--AVGNT--AVN---RC--KDANGNVY--KNCRN-AG-SAD-VYV 94  
134 NWTAWSEDGNGTGQSHHNVFPDGKPPHHPGWRWNIYVYVHTLQYFQKLGRCVSR 193  
95 NWTAW--DSDG-NGTG-SHNV--DGK---HGWRRWNYVHTGYK-----GRCSVR 137  
194 VSVNTANVTLGQPMVEVTVRRHGRAYVPIAOKDVVYVTDQIPVFTVTFQKNDNSDE 253  
138 VSVNTANVT-----GMVTVRRHGRAYV--AVKDVVVVTD---VVTM--KNDNSD 183  
254 TFLKDLPIMDVLHDPHFNLNYSTINYKWSFGDNTGLFVSTNHTVNTHTVYVLTGFS 313  
184 K-----DMDVHD-SH--NYST-NYKWS-GDNTG--VSTNHTVNTHTVYV-NGTSN--- 223  
314 TVKAAAPGCPPPPPPPRPSKPTSLGPDAGNPLESRIPDENQINRYGHFOATITVE 373  
224 TVKAAA--GC-----RSKTSAGDN-----SR-----DNC--NRYGH---ATTVG 256  
374 GILEVNIQMTDVLMPVPWPESSLIQVTCOGSIPTVCTIISDPTCEITONTVCSPVD 433  
257 -----VNMTDMV-----WSSD-----VVC-GS-----TVCTSDTC---TNTVCS-VD 290  
434 VDEMCLLTVRTFNQSGTYCVNLTGLDSTLSTLISVPRDRDPASPLRMANSALISVG 493  
291 VD-MC--TVRRT-NGSGTYCVN--TGDDTSATSTSV-----DRDAS---RMANSA--SVG 334  
494 CLAIPTVVISLLVYKHKKEYPNIENSPGNVRSKGLSVFLNRAKAVFPFGNQEKDPLKN 553  
335 C-----AVTSVYKHK-----YNSGNVRSKG---SVNRAKAV---GNKDKN----- 372  
554 QEFKGS 560  
373 ---KGVS 376

RESULT 15  
US-09-977-371-100  
Sequence 100, Application US/09977371  
Patent No. RE38490  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/977,371  
FILING DATE: 16-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 100:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 100:  
US-09-977-371-100

Query Match 32.0%; Score 969; DB 1; Length 376;  
Best Local Similarity 54.5%; Pred. No. 1.8e-80;  
Matches 298; Conservative 26; Mismatches 47; Indels 176; Gaps 60;

14 AARPLDAAKRFHDLGNRPSAYMRHNLQNGSSDNDWNEKLYPVWKGDMRWKNSW 73  
6 AAR---DAKR-HDV-GNR--SAYMR-HN--NGWSSD-NDWNY---VWKGDMRWKNSW 51  
74 KGRVQAVLTSDSPALVGSNITFAVNLIFPRCQKEDANGNIYVYKNCNEAGLSADPYVY 133  
52 KGRV--AVTSDS--AVGNT--AVN---RC--KDANGNVY--KNCRN-AG-SAD-VYV 94  
134 NWTAWSEDGNGTGQSHHNVFPDGKPPHHPGWRWNIYVYVHTLQYFQKLGRCVSR 193  
95 NWTAW--DSDG-NGTG-SHNV--DGK---HGWRRWNYVHTGYK-----GRCSVR 137  
194 VSVNTANVTLGQPMVEVTVRRHGRAYVPIAOKDVVYVTDQIPVFTVTFQKNDNSDE 253  
138 VSVNTANVT-----GMVTVRRHGRAYV--AVKDVVVVTD---VVTM--KNDNSD 183  
254 TFLKDLPIMDVLHDPHFNLNYSTINYKWSFGDNTGLFVSTNHTVNTHTVYVLTGFS 313  
184 K-----DMDVHD-SH--NYST-NYKWS-GDNTG--VSTNHTVNTHTVYV-NGTSN--- 223  
314 TVKAAAPGCPPPPPPPRPSKPTSLGPDAGNPLESRIPDENQINRYGHFOATITVE 373  
224 TVKAAA--GC-----RSKTSAGDN-----SR-----DNC--NRYGH---ATTVG 256  
374 GILEVNIQMTDVLMPVPWPESSLIQVTCOGSIPTVCTIISDPTCEITONTVCSPVD 433  
257 -----VNMTDMV-----WSSD-----VVC-GS-----TVCTSDTC---TNTVCS-VD 290  
434 VDEMCLLTVRTFNQSGTYCVNLTGLDSTLSTLISVPRDRDPASPLRMANSALISVG 493  
291 VD-MC--TVRRT-NGSGTYCVN--TGDDTSATSTSV-----DRDAS---RMANSA--SVG 334

Qy 494 CLAIPTVISLLVYKXKHEYNPIENSPGNVVRSGLSVFLNRAKAVFFPGNOEKDPLLKN 553  
Db 335 C-----AVTVSVYKHK-----YNSGNVVRSG---SVNRAKAV---GNKDKN----- 372  
Qy 554 QEFKGV 560  
Db 373 ---RGVS 376

Search completed: November 19, 2004, 15:00:38  
Job time : 41 secs